

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Date completed: <u>01-14-03</u>	Search Site	Vendors
Searcher: <u>Beverly C. 4411</u>	<u>STIC</u>	<u>IG</u>
Terminal time: <u>20 2528</u>	<u>CM-1</u>	<u>STN</u>
Elapsed time: _____	<u>Pre-S</u>	<u>Dialog</u>
CPU time: _____	Type of Search	<u>APS</u>
Total time: <u>25</u>	<u>N.A. Sequence</u>	<u>Geninfo</u>
Number of Searches: _____	<u>A.A. Sequence</u>	<u>SDC</u>
Number of Databases: <u>1</u>	<u>Structure</u>	<u>DARC/Questel</u>
	<u>Bibliographic</u>	<u>Other CGN</u>

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2004, 15:53:18 ; Search time 744 Seconds
(without alignments)
1044.735 Million cell updates/sec

Title: US-09-719-737-18

Perfect score: 19

Sequence: 1 ctgggccatcagtcctctg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2886711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
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13: gb_un:*
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16: em_fun:*
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28: em_un:*
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32: em_htg_other:*
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34: em_htg_pln:*
35: em_htg_rod:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	6	AX008665
2	19	100.0	19	6	AX008666
3	19	100.0	19	6	AX671175
4	19	100.0	260	9	AF224495
5	19	100.0	348	9	AF262299
6	19	100.0	406	9	AF262301
7	19	100.0	410	9	AF262302
8	19	100.0	1065	6	ARI64119
9	19	100.0	1065	6	AX030929
10	19	100.0	1065	6	BD128569
11	19	100.0	1068	6	AX280851
12	19	100.0	1068	6	AX323054
13	19	100.0	1068	9	AB023887
14	19	100.0	1068	9	AF026535
15	19	100.0	1068	9	AY221092
16	19	100.0	1071	6	AR278855
17	19	100.0	1071	6	BD015209
18	19	100.0	1116	6	AR300123
19	19	100.0	1116	6	BD082062
20	19	100.0	1193	6	AR300122
21	19	100.0	1193	6	BD082061
22	19	100.0	1201	6	AR270522
23	19	100.0	1201	6	AX548778
24	19	100.0	1201	9	HSU28694
25	19	100.0	1310	9	AF262300
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28	19	100.0	1689	9	HSU49727
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33	19	100.0	2030	9	BC033514
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ALIGNMENTS

RESULT 1
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LOCUS AX008665
DEFINITION Sequence 18 from Patent WO9966037.
ACCESSION AX008665
VERSION AX008665.1 GI:9996189
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Renzi, P.
TITLE Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
JOURNAL Patent: WO 9966037-A 18 23-DEC-1999;

RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
location/Qualifiers
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RESULT 2
AX008666/c 19 bp DNA linear PAT 06-SEP-2000
LOCUS Sequence 19 from Patent WO9966037.
ACCESSION AX008666
VERSION AX008666.1 GI:9996190
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Renzi, P.
TITLE Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
JOURNAL Patent: WO 9966037-A 19 23-DEC-1999;
RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
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AX671175 19 bp DNA linear PAT 27-MAR-2003
LOCUS Sequence 15 from Patent WO03004511.
ACCESSION AX671175
VERSION AX671175.1 GI:29329631
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Renzi, P., Allam, M. and Allakhverdi, Z.
TITLE Methods for increasing in vivo efficacy of oligonucleotides and inhibiting inflammation in mammals
JOURNAL Patent: WO 03004511-A 15 16-JAN-2003;
Topigen Pharmaceuticals Inc (CA)
location/Qualifiers
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AF224495/c 260 bp mRNA linear PRI 02-MAY-2001
LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.
DEFINITION AF224495
ACCESSION AF224495
VERSION AF224495.1 GI:13924481
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 260)
AUTHORS Scotet, E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2 cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 260)
AUTHORS Scotet, E.J.
TITLE Direct Submision
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487 Grenzacherstrasse, Basel CH-4005, Switzerland
location/Qualifiers
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OY 1 CTGGGCCATCAGTGTCTG 19
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Db 195 CTGGGCCATCAGTGTCTG 177

RESULT 5
AF262299/c 348 bp mRNA linear PRI 26-JUN-2002
LOCUS Homo sapiens clone 1 CC chemokine receptor 3 (CCR3) mRNA, partial cds.
DEFINITION AF262299
ACCESSION AF262299
VERSION AF262299.1 GI:19171640
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
REFERENCE Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
AUTHORS 1 (bases 1 to 348)
Vijh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
REFERENCE 2 (bases 1 to 348)
AUTHORS Vijh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA
FEATURES
source Location/Qualifiers
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QY 1 CTGGCCATCAGTCTCTG 19
Db 224 CTGGCCATCAGTCTCTG 206
RESULT 6
AF262301/c
LOCUS Homo sapiens clone 4 CC chemokine receptor 3 (CCR3) mRNA, partial cds.
DEFINITION AF262301
AF262301 406 bp mRNA linear PRI 26-JUN-2002
AF262301.1 GI:19171644
ACCESSION AF262301
VERSION AF262301.1 GI:19171644
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
AUTHORS 1 (bases 1 to 406)
Vijh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933

PUBMED 12079287
REFERENCE 2 (bases 1 to 406)
AUTHORS Vijh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGCCATCAGTCTCTG 19
Db 264 CTGGCCATCAGTCTCTG 246
RESULT 7
AF262302/c
LOCUS Homo sapiens clone 5 CC chemokine receptor 3 (CCR3) mRNA, partial cds.
DEFINITION AF262302
AF262302 410 bp mRNA linear PRI 26-JUN-2002
AF262302.1 GI:19171646
ACCESSION AF262302
VERSION AF262302.1 GI:19171646
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
AUTHORS 1 (bases 1 to 410)
Vijh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
REFERENCE 2 (bases 1 to 410)
AUTHORS Vijh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGGGCCATCAGTGCTCTG 19
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Db      274 CTGGGCCATCAGTGCTCTG 256

RESULT 8
ARI64119/c
LOCUS      ARI64119      1065 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION Sequence 2 from patent US 6271347.
ACCESSION  ARI64119
VERSION     ARI64119.1 GI:16235065
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 1065)
AUTHORS    Daugherty,B.L., Demartino,J.A., Siciliano,S.J. and Springer,M.S.
TITLE      Eosinophil eotaxin receptor
JOURNAL    Patent: US 6271347-A 2 07-AUG-2001;
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QY      1 CTGGGCCATCAGTGCTCTG 19
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Db      105 CTGGGCCATCAGTGCTCTG 87

RESULT 9
AX030929/c
LOCUS      AX030929      1065 bp      DNA      linear      PAT 20-SEP-2000
DEFINITION Sequence 2 from Patent EP1012190.
ACCESSION  AX030929
VERSION     AX030929.1 GI:10278334
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1
AUTHORS    Daugherty,B.L., Demartino,J.A., Siciliano,S.J. and Springer,M.S.
TITLE      Eosinophil eotaxin receptor
JOURNAL    Patent: EP 1012190-A 2 28-JUN-2000;
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MERCK & CO INC (US)
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Db      105 CTGGGCCATCAGTGCTCTG 87

RESULT 10
BD128569/c
LOCUS      BD128569      1065 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Eosinophil eotaxin receptor.
ACCESSION  BD128569
VERSION     BD128569.1 GI:23223514
KEYWORDS    JP 2002503950-A/1.
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 1065)
AUTHORS    Daugherty,B.L., Demartino,J.A., Springer,M.S. and Siciliano,S.J.
TITLE      Eosinophil eotaxin receptor
JOURNAL    Patent: JP 2002503950-A 1 05-FEB-2002;
COMMENT     MERCK & CO INC
OS          Unidentified
PN          JP 2002503950-A/1
PD          05-FEB-2002
PF          24-APR-1997 JP 1997538970
PR          26-APR-1996 US 08/640991,26-APR-1996 US 60/016158 PR
PI          17-JAN-1997 GB 9700894.0
PI          BRUCE L DAUGHERTY,JULIE A DEMARTINO,MARTIN S SPRINGER PI
PC          SALVATORE J SICILIANO
PC          C07K14/705,C07K14/715,C12N15/12
CC          Strandedness: Single;
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      105 CTGGGCCATCAGTGCTCTG 87

RESULT 11
AX280851/c
LOCUS      AX280851      1068 bp      DNA      linear      PAT 02-NOV-2001
DEFINITION Sequence 474 from Patent WO0177172.
ACCESSION  AX280851
VERSION     AX280851.1 GI:16608181
KEYWORDS
SOURCE      Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1
AUTHORS Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.
TITLE Non-endogenous, constitutively activated known g protein-coupled receptors
JOURNAL Patent: WO 0177172-A 474 18-OCT-2001;
Arena Pharmaceuticals, Inc. (US)
FEATURES
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Db 105 CTGGCCATCAGTCTCTG 87
RESULT 12
AX323054/c 1068 bp DNA linear PAT 07-JAN-2002
LOCUS Sequence 2 from Patent WO0192520.
DEFINITION AX323054
ACCESSION AX323054
VERSION AX323054.1 GI:18093940
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1
AUTHORS Barnes, A.A., Fraser, N.J., O'Shaughnessy, C.T. and Wise, A.G.
TITLE Modified chemokine receptor ccr-3 and assay
JOURNAL Patent: WO 0192520-A 2 06-DEC-2001;
GLAXO GROUP LIMITED (GB)
FEATURES
Source Location/Qualifiers
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RESULT 13
AB023887/c

LOCUS AB023887 1068 bp DNA linear PRI 25-NOV-1999
DEFINITION Homo sapiens gene for b-chemokine receptor CCR3, complete cds.
ACCESSION AB023887
VERSION AB023887.1 GI:6467132
KEYWORDS b-chemokine receptor CCR3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1
AUTHORS Kato, H., Tsuchiya, N., Izumi, S., Miyamasu, M., Nakajima, T.,
Kawabaki, H., Hirai, K. and Tokunaga, K.
TITLE New variations of human CC-chemokine receptors CCR3 and CCR4
JOURNAL Genes Immun. 1 (2), 97-104 (1999)
MEDLINE 21040311
PUBMED 11196669
REFERENCE 2 (bases 1 to 1068)
AUTHORS Kato, H., Tsuchiya, N. and Tokunaga, K.
TITLE Direct Submision
JOURNAL Submitted (19-FEB-1999) Hitoshi Kato, University of Tokyo,
Department of Human Genetics; 7-3-1 Hongo, Bunkyo-ku, Tokyo
113-0033, Japan (E-mail: katoch@u-tokyo.ac.jp, Tel:81-3-5841-3542,
Fax:81-3-5802-8619)
FEATURES
Source Location/Qualifiers
1.1068
/organism="Homo sapiens"
/mol_type="genomic DNA"
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/chromosome="3"
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1.1068
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/protein_id="BA86964.1"
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VTGIILKLRCPSSKKYKAIKRLIFVIMAVFPIFMTPTNVAIILSSYOSILEGNDCERT
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BASE COUNT 232 a 289 c 243 g 304 t
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGCCATCAGTCTCTG 19
Db 105 CTGGCCATCAGTCTCTG 87
RESULT 14
AF026535/c 1068 bp mRNA linear PRI 02-NOV-1997
LOCUS AF026535
DEFINITION Homo sapiens chemokine receptor (CCR3) mRNA, complete cds.
ACCESSION AF026535
VERSION AF026535.1 GI:2582565
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1 (bases 1 to 1068)
AUTHORS Xiao, L., Weiss, S., Qari, S., Rudolph, D., Hodge, T. and Lal, R.
TITLE Partial resistance to infection by syncytium-inducing primary HIV-1
JOURNAL in exposed uninfected individuals homozygous for CCR5 32bp deletion
REFERENCE 2 (bases 1 to 1068)

AUTHORS Qari, S.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1997) Retrovirus Diseases Branch, Centers for Disease Control and Prevention, 1600 Clifton Road, Atlanta, GA 30333, USA

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BASE COUNT 231 a 289 c 243 g 305 t
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTGCTCTG 19
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105 CTGGGCCATCAGTGCTCTG 87

Db 105 CTGGGCCATCAGTGCTCTG 87

RESULT 15
AY221092/c 1068 bp DNA linear PRI 11-APR-2003
LOCUS Homo sapiens chemokine receptor 3 gene, complete cds.
DEFINITION AY221092
ACCESSION AY221092
VERSION AY221092.1 GI:29169288
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1068)
AUTHORS Kopatz, S.A., Aronstam, R.S. and Sharma, S.V.
TITLE Isolation of complete coding sequence for chemokine (C-C motif) receptor 3 (CCR3)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1068)
AUTHORS Kopatz, S.A., Aronstam, R.S. and Sharma, S.V.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-2003) Guthrie CDNA Resource Center, Guthrie Research Institute, 1 Guthrie Square, Sayre, PA 18840, USA

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/db_xref="GI:29169289"

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BASE COUNT 231 a 288 c 243 g 306 t
ORIGIN

Query Match 100.0%; Score 19; DB 9; Length 1068;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTGCTCTG 19
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105 CTGGGCCATCAGTGCTCTG 87

Db 105 CTGGGCCATCAGTGCTCTG 87

RESULT 16
AR278855/c 1071 bp mRNA linear PAT 10-APR-2003
LOCUS AR278855
DEFINITION Sequence 6 from patent US 6512103.
ACCESSION AR278855
VERSION AR278855.1 GI:29713353
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1071)
AUTHORS Dairaghi, D.J., Hara, T., Miyajima, A., Schall, T.J., Wang, W. and Yoshimura, A.
TITLE Mammalian chemokine reagents
JOURNAL Patent: US 6512103-A 6 28-JAN-2003;
FEATURES location/Qualifiers
source 1. 1071
/organism="unknown"

BASE COUNT 231 a 292 c 242 g 306 t
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTGCTCTG 19
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105 CTGGGCCATCAGTGCTCTG 87

Db 105 CTGGGCCATCAGTGCTCTG 87

RESULT 17
BD015209/c 1071 bp DNA linear PAT 27-AUG-2002
LOCUS Mammalian chemokine CCR18 and receptor CCR3 of mammal.
DEFINITION BD015209
ACCESSION BD015209
VERSION BD015209.1 GI:22556016
KEYWORDS JP 2001157593-A/4.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1071)
AUTHORS Dairaghi, D.J., Hara, T., Miyajima, A., Schall, T.J., Wan, W. and Yoshimura, A.
TITLE Mammalian chemokine CCR18 and receptor CCR3 of mammal
JOURNAL Patent: JP 2001157593-A 4 12-JUN-2001;
COMMENT SCHERING CORP
OS Unidentified
PN JP 2001157593-A/4
PD 12-JUN-2001
PF 04-OCT-2000 JP 2000305562
PR 08-DEC-1995 US 08/567882
PI DANIEL J DAIRAGHI, TAKAHIKO HARA, ATSUSHI MIYAJIMA, THOMAS J PI SCHALL, WEI WANG, AKIHIKO YOSHIMURA

PC C12N15/09,C07K14/715,C07K16/28,C07K19/00,C12P21/02,C12P21/08//
PC C12N5/10,
PC C12N15/00,C12N5/00
CC Strandedness: Single;
CC Topology: linear;
CC Mammalian chemokine CCR18 and receptor CCR3 of mammal FH
Key Location/Qualifiers
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BASE COUNT 231 a 292 c 242 g 306 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTCTCTG 19
Db 105 CTGGGCCATCAGTCTCTG 87
RESULT 18
AR300123/c 1116 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 5 from patent US 6537764.
ACCESSION AR300123
VERSION AR300123.1 GI:31687432
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1116)
AUTHORS Gerard,C.J., Gerard,N.P., Mackay,C.R., Ponath,P.D., Post,T.W. and Qin,S.
TITLE Method of identifying inhibitors of C--C chemokine receptor 3
JOURNAL Patent: US 6537764-A 5 25-MAR-2003;
FEATURES
source 1..1116
/organism="unknown"
BASE COUNT 246 a 286 c 257 g 306 t 21 others
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTCTCTG 19
Db 119 CTGGGCCATCAGTCTCTG 101
RESULT 19
BD082062/c 1116 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION G-protein coupled receptor antagonists.
ACCESSION BD082062
VERSION BD082062.1 GI:22627672
KEYWORDS JP 2001524068-A/3.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1116)
AUTHORS Mackay,C.R. and Ponath,P.D.
TITLE G-protein coupled receptor antagonists
JOURNAL Patent: JP 2001524068-A 3 27-NOV-2001;
LEUKOSITE INC
COMMENT PN JP 2001524068-A/3

PD 27-NOV-2001
PF 24-SEP-1997 JP 1998516642
PR 30-SEP-1996 US 08/720565
PI CHARLES R MACKAY, PAUL D PONATH
PC C07K16/18,C07K16/28,A61K39/395
CC Strandedness: Double;
CC Topology: linear;
Key Location/Qualifiers
FH Key 1..1116
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source 1..1116
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/mol_type="genomic DNA"
/db_xref="taxon:4577"
BASE COUNT 246 a 286 c 257 g 306 t 21 others
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTCTCTG 19
Db 119 CTGGGCCATCAGTCTCTG 101
RESULT 20
AR300122/c 1193 bp mRNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 3 from patent US 6537764.
ACCESSION AR300122
VERSION AR300122.1 GI:31687431
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1193)
AUTHORS Gerard,C.J., Gerard,N.P., Mackay,C.R., Ponath,P.D., Post,T.W. and Qin,S.
TITLE Method of identifying inhibitors of C--C chemokine receptor 3
JOURNAL Patent: US 6537764-A 3 25-MAR-2003;
FEATURES
source 1..1193
/organism="unknown"
BASE COUNT 274 a 310 c 275 g 334 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTCTCTG 19
Db 196 CTGGGCCATCAGTCTCTG 178
RESULT 21
BD082061/c 1193 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION G-protein coupled receptor antagonists.
ACCESSION BD082061
VERSION BD082061.1 GI:22627671
KEYWORDS JP 2001524068-A/2.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1193)
AUTHORS Mackay,C.R. and Ponath,P.D.
TITLE G-protein coupled receptor antagonists
JOURNAL Patent: JP 2001524068-A 2 27-NOV-2001;
LEUKOSITE INC
COMMENT PN JP 2001524068-A/2

PD 27-NOV-2001
PF 24-SEP-1997 JP 1998516642
PR 30-SEP-1996 US 08/720565
PI CHARLES R MACKAY, PAUL D PONATH
PC C07K16/18, C07K16/28, A61K39/395
CC Strandedness: Double;
CC Topology: Linear;
FH Key CDS Location/Qualifiers
FT 92.1156.
Source 1.1193
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BASE COUNT 274 a 310 c 275 g 334 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 1193;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
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Db 196 CTGGGCCATCAGTCTCTG 178

RESULT 22
AR270522/c 1201 bp DNA linear PAT 10-APR-2003
LOCUS AR270522
DEFINITION Sequence 1085 from patent US 6500938.
ACCESSION AR270522
VERSION AR270522.1 GI:29701756
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Au-Young, J. and Seilhamer, J. J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1085 31-DEC-2002;
FEATURES
Source 1.1201
Location/Qualifiers
BASE COUNT 278 a 320 c 267 g 336 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 1201;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
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Db 136 CTGGGCCATCAGTCTCTG 118

RESULT 23
AX548778/c 1201 bp DNA linear PAT 26-NOV-2002
LOCUS AX548778
DEFINITION Sequence 63 from Patent WO02061087.
ACCESSION AX548778
VERSION AX548778.1 GI:25813697
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Burner, G. C., Roush, C. L. and Brown, J. P.
TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides
JOURNAL Patent: WO 02061087-A 63 08-AUG-2002;
Lifespan Biosciences, Inc. (US)

FEATURES Location/Qualifiers
Source 1.1201
/organism="Homo sapiens"
/mol_type="genomic DNA"
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BASE COUNT 278 a 320 c 267 g 336 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 1201;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
|||||
Db 136 CTGGGCCATCAGTCTCTG 118

RESULT 24
HSU28694/c 1201 bp mRNA linear PRI 16-MAY-1996
LOCUS HSU28694
DEFINITION Human eosinophil CC chemokine receptor 3 mRNA, complete cds.
ACCESSION U28694
VERSION U28694.1 GI:1199579
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1200)
AUTHORS Combadiere, C., Ahuja, S. K. and Murphy, P. M.
TITLE Cloning and functional expression of a human eosinophil CC chemokine receptor
JOURNAL J. Biol. Chem. 270 (28), 16491-16494 (1995)
MEDLINE 95348056
PUBMED 7622448
REFERENCE 2 (bases 1 to 1201)
AUTHORS Combadiere, C.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-1995) Christophe Combadiere, NIAID, National Institutes of Health, Building 10, Room 11N11, Bethesda, MD 20892, USA
REFERENCE 3 (bases 1 to 1201)
AUTHORS Combadiere, C., Ahuja, S. K. and Murphy, P. M.
TITLE Cloning and functional expression of a human eosinophil CC chemokine receptor
JOURNAL J. Biol. Chem. 271 (18), 11034 (1996)
MEDLINE 96210048
PUBMED 8631926
COMMENT On Feb 22, 1996 this sequence version replaced gi:861569.
[Erratum J. Biol. Chem. 270 (1995) 30235].
FEATURES
Source 1.1201
Location/Qualifiers
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/organism="Homo sapiens"
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/cell_type="eosinophil"
32.1099
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/db_xref="GI:1199580"
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BASE COUNT 278 a 320 c 267 g 336 t
ORIGIN

Query Match 100.0%; Score 19; DB 9; Length 1201;
Best Local Similarity 100.0%; Pred. No. 14;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
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136 CTGGCCATCAGTCTCTG 118

RESULT 25
AF262300/c
LOCUS AF262300 1310 bp mRNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens clone 2 CC chemokine receptor 3 (CCR3) mRNA, partial cds.
ACCESSION AF262300
VERSION AF262300.1 GI:19171642
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1310)
Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
AUTHORS
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
REFERENCE 2 (bases 1 to 1310)
Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA

FEATURES
source
1. 1310
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/gene="CCR3"
/note="G-protein coupled receptor; principal eotaxin receptor expressed on eosinophils, CD4 Th2 lymphocytes, CD8 lymphocytes, microglia, dendritic cells, and monocytes"
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/db_xref="GI:19171643"
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BASE COUNT 350 a 317 c 260 g 383 t
ORIGIN

Query Match 100.0%; Score 19; DB 9; Length 1310;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
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1208 CTGGCCATCAGTCTCTG 1190

RESULT 26
AR300121/c
LOCUS AR300121 1689 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1 from patent US 6537764.

ACCESSION AR300121
VERSION AR300121.1 GI:31687430
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1689)
AUTHORS Gerard,C.J., Gerard,N.P., Mackay,C.R., Ponath,P.D., Post,T.W. and Qin,S.
TITLE Method of identifying inhibitors of C--C chemokine receptor 3
JOURNAL Patent: US 6537764-A 1 25-MAR-2003;
FEATURES
source
1. 1689
/organism="unknown"
BASE COUNT 431 a 416 c 344 g 497 t 1 others
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 1689;
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
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285 CTGGCCATCAGTCTCTG 267

RESULT 27
BD082060/c
LOCUS BD082060 1689 bp DNA linear PAT 27-AUG-2002
DEFINITION G-protein coupled receptor antagonists.
ACCESSION BD082060
VERSION BD082060.1 GI:22627670
KEYWORDS JP 2001524068-A/1.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1689)
Mackay,C.R. and Ponath,P.D.
AUTHORS
TITLE G-protein coupled receptor antagonists
JOURNAL Patent: JP 2001524068-A 1 27-NOV-2001;
COMMENT
PN JP 2001524068-A/1
PD 27-NOV-2001
PF 24-SEP-1997 JP 1998516642
PR 30-SEP-1996 US 08/720565
PI CHARLES.R MACKAY,PAUL D PONATH
PC C07K16/18,C07K16/28,A61K39/395
CC Strandedness: Double;
CC Topology: Linear;
FH Key
FEATURES
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/db_xref="taxon:4577"
BASE COUNT 431 a 416 c 344 g 497 t 1 others
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 1689;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
|||||
285 CTGGCCATCAGTCTCTG 267

RESULT 28
HSU49727/c
LOCUS HSU49727 1689 bp DNA linear PRI 04-OCT-1996
DEFINITION Human C-C chemokine receptor 3 (CCR-3) gene, complete cds.

ACCESSION U49727 GI:1477560
VERSION U49727.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1689)
AUTHORS Ponath, P.D., Qin, S., Post, T.W., Wang, J., Wu, L., Gerard, N.P.,
Newman, W., Gerard, C. and Mackay, C.R.
TITLE Molecular cloning and characterization of a human eosinophil
expressed selectively on eosinophils
JOURNAL J. Exp. Med. 183 (6), 2437-2448 (1996)
MEDLINE 96281895
PUBMED 8676064
REFERENCE 2 (bases 1 to 1689)
AUTHORS Ponath, P.D.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-1996) Paul D. Ponath, Molecular Biology,
Leukocyte, Inc., 215 First St., Cambridge, MA 02118, USA
FEATURES
source 1..1689
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/db_xref="taxon:9606"
1..1689
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181..1248
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and MCP-3"
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/product="C-C chemokine receptor 3"
/protein_id="AAB09726.1"
/db_xref="GI:1477561"
/translation="MTSLDVTETFGTTSYDDVGLCEKADTRALMAQFVPLYSIV
FTVGLGNVVVMILIKRRRLRIMNTIYLNLAISDLFLVTLPMIHVYRGHNWVG
HGMCKLSGFYHTGLYSEIFIILITIDRYLAIVHAVFALRARTVFGVITSIVTWGL
AVLAALPERIFYETBELFEETLCSALYPEDTVYSWRHFTLMTIFCLVPLLVMAIC
VTGIITLRCPSKKYKAIRLIFVIMAVFIFWTPYNAVALISSYOSILFGNDCERT
KHLDLVMLVTEVIAYSHCCMNPVIYAFVGBRRKYLRRHFRHLLMLGRYIPFLPSE
KLERTSSVSPSTABPELSIVF"
BASE COUNT 430 a 416 c 345 g 497 t 1 others
ORIGIN
Query Match 100.0%; Score 19; DB 9; Length 1689;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTGTCTG 19
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Db 285 CTGGGCCATCAGTGTCTG 267
RESULT 29
AX334894/c 1717 bp DNA linear PAT 09-JAN-2002
LOCUS AX334894
DEFINITION Sequence 5403 from Patent WO0194629.
ACCESSION AX334894
VERSION AX334894.1 GI:18125613
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 5403 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
Location/Qualifiers

source 1..1717
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 434 a 428 c 351 g 504 t
ORIGIN
Query Match 100.0%; Score 19; DB 6; Length 1717;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTGTCTG 19
|||
Db 309 CTGGGCCATCAGTGTCTG 291
RESULT 30
HSU51241/c 1717 bp DNA linear PRI 09-OCT-1996
LOCUS HSU51241
DEFINITION Human eosinophil eotaxin receptor (CMKBR3) gene, complete cds.
ACCESSION U51241
VERSION U51241.1 GI:1480480
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1717)
AUTHORS Daugherty, B.L., Siciliano, S.J., DeMartino, J.A., Malkowitz, L.,
Strotina, A. and Springer, M.S.
TITLE Cloning, expression, and characterization of the human eosinophil
eotaxin receptor
JOURNAL J. Exp. Med. 183 (5), 2349-2354 (1996)
MEDLINE 96235044
PUBMED 8642344
REFERENCE 2 (bases 1 to 1717)
AUTHORS Daugherty, B.L.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-1996) Bruce L. Daugherty, Inflammation Research,
Merck Research Laboratories, R80W-107, P.O. Box 2000, Rahway, NJ
07065, USA
FEATURES
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205..1272
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205..1272
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/note="CC chemokine receptor-3; CCR3"
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/protein_id="AAB16831.1"
/db_xref="GI:1480481"
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AVLAALPERIFYETBELFEETLCSALYPEDTVYSWRHFTLMTIFCLVPLLVMAIC
VTGIITLRCPSKKYKAIRLIFVIMAVFIFWTPYNAVALISSYOSILFGNDCERS
KHLDLVMLVTEVIAYSHCCMNPVIYAFVGBRRKYLRRHFRHLLMLGRYIPFLPSE
KLERTSSVSPSTABPELSIVF"
BASE COUNT 434 a 428 c 351 g 504 t
ORIGIN
Query Match 100.0%; Score 19; DB 9; Length 1717;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTGTCTG 19
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Db 309 CTGGGCCATCAGTGTCTG 291


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RESULT 31
BD006761/c
LOCUS BD006761 1915 bp DNA linear PAT 31-JAN-2002
DEFINITION Chemokine receptors 88-2B [CKR-3] and 88C and antibodies thereof.
ACCESSION BD006761
VERSION BD006761.1 GI:18635132
KEYWORDS JP 2001029089-A/2.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1915)
AUTHORS Gary, P.W., Sheikart, V.L. and Rayport, C.J.
TITLE Chemokine receptors 88-2B [CKR-3] and 88C and antibodies thereof
JOURNAL Patent: JP 2001029089-A 2 06-FEB-2001;
COMMENT
OS Unidentified
PN JP 2001029089-A/2
PD 06-FEB-2001
PF 16-MAY-2000 JP 2000143832
PR 20-DEC-1995 US 08/575967, 07-JUN-1996 US 08/661393 PI
PATRICK W GARY, VICWIKI L SHEIKART, CARROLL J RAYPORT PC
C12N15/09, C07K14/715, C07K16/24, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12N5/10, C12N15/02, C12P21/02, C12P21/08, C12Q1/68, G01N33/15, PC
G01N33/50,
PC G01N33/53, G01N33/566//A61K39/395, A61K39/395, A61K45/00, A61P7/02, PC
A61P17/06,
PC A61P19/02, A61P29/00, A61P31/12, (C12P21/02, C12R1:91), C12N15/00,
PC C12N5/00, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 362..1426.
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BASE COUNT 488 a 470 c 373 g 584 t
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGGGCCATCAGTCTCTG 19
Db 466 CTGGGCCATCAGTCTCTG 448
RESULT 32
BD017703/c
LOCUS BD017703 1915 bp DNA linear PAT 27-AUG-2002
DEFINITION Chemokine receptors 88-2B [CKR-3] and 88C, and antibodies thereof.
ACCESSION BD017703
VERSION BD017703.1 GI:22558879
KEYWORDS JP 2001264324-A/2.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1915)
AUTHORS Gary, P.W., Schweickart, V.L. and Raport, C.J.
TITLE Chemokine receptors 88-2B [CKR-3] and 88C, and antibodies thereof
JOURNAL Patent: JP 2001264324-A 2 26-SEP-2001;
COMMENT
OS Unidentified
PN JP 2001264324-A/2
PD 26-SEP-2001
PF 28-DEC-2000 JP 2000401708
PR 20-DEC-1995 US 08/575967, 07-JUN-1996 US 08/661393 PI

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PATRICK W GARY, VICKI L SCHWEICKART, CARROLL J RAPORT PC
G01N33/50, A61K38/00, A61K45/00, A61P31/12, A61P31/18, C12Q1/02, PC
C12Q1/70,
PC G01N33/15, G01N33/566, G01N33/569//C07K14/705, C07K16/28, C12N15/
PC 09, C12P21/02,
PC C12P21/08, (C12Q1/02, C12R1:91), (C12Q1/70, C12R1:93), (C12P21/02,
PC C12R1:91),
PC A61K37/02, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC /= 88-2B polynucleotide and amino acid sequence' FH Key
FT CDS 362..1426.
FEATURES
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/organism="unclassified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 488 a 470 c 373 g 584 t
ORIGIN
Query Match 100.0%; Score 19; DB 6; Length 1915;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTGGGCCATCAGTCTCTG 19
Db 466 CTGGGCCATCAGTCTCTG 448
RESULT 33
BC033514/c
LOCUS BC033514 2030 bp mRNA linear PRI 17-OCT-2002
DEFINITION Homo sapiens, similar to chemokine (C-C motif) receptor 3, clone
MGC:34625 IMAGE:5176960, mRNA, complete cds.
ACCESSION BC033514
VERSION BC033514.1 GI:23958837
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2030)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunsaratne, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Louised, H.,
Kowis, C.R., Sneed, A.U., Martin, R.G., Muzny, D.M., Navavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAX Plate: 51 Row: n Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4502636.
FEATURES
source 1. 2030
/organism="Homo sapiens"
/mol_type="mRNA"

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		/lab_host="DH10B"	
		/note="Vector: pCMV-SPORT6"	
CDS		544..1611	
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		/db_xref="LocusID:1232"	
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		AVLAALPEFI FYETELFEETLCSALYPEDTVYSWRHFHRLMTIFCLVPLLVMAIC	
		YTGIITKLRCPSKKKYKAIRLIFVIMAVFEI FWT PYNVAIILSSYQSLFGNDCERS	
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BASE COUNT		537 a	519 c 446 g 528 t
ORIGIN			
Query Match		100.0%;	Score 19; DB 9; Length 2030;
Best Local Similarity		100.0%;	Pred. No. 14;
Matches		19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY		1	CTGGGCCATCAGTGTCTG 19
Db		648	CTGGGCCATCAGTGTCTG 630
RESULT 34			
AX705064/c		5791 bp	DNA linear PAT 04-APR-2003
LOCUS			
DEFINITION		Sequence 5 from Patent WO03014153.	
ACCESSION		AX705064	
VERSION		AX705064.1 GI:29561706	
KEYWORDS			
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1	Renzi, P., Zemzoui, K. and Lankhouned, B.
AUTHORS		Cellular virus receptors and methods of use	
TITLE		Patent: WO 03014153-A 5 20-FEB-2003;	
JOURNAL		Topigen Pharmaceutique Inc (CA)	
FEATURES		location/Qualifiers	
source		1..5791	
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		4015..5082	
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		AVLAALPEFI FYETELFEETLCSALYPEDTVYSWRHFHRLMTIFCLVPLLVMAIC	
		YTGIITKLRCPSKKKYKAIRLIFVIMAVFEI FWT PYNVAIILSSYQSLFGNDCERS	
		KHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKYLRRHFFHRHLLMHLGRYIPFLPSE	
		KLERTSSVSPSTAPELSIV"	
BASE COUNT		1624 a	1285 c 1160 g 1722 t
ORIGIN			
Query Match		100.0%;	Score 19; DB 6; Length 5791;
Best Local Similarity		100.0%;	Pred. No. 15;
Matches		19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY		1	CTGGGCCATCAGTGTCTG 19

RESULT 35	AF247361/c	5791 bp	DNA	linear	PRI 26-JUN-2002
LOCUS	Homo sapiens CC chemokine receptor 3 (CCR3) gene, complete cds.				
DEFINITION	AF247361				
ACCESSION	AF247361.1 GI:19110542				
VERSION	AF247361.1				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 5791)				
AUTHORS	Vijh, S., Dayhoff, D.E., Wang, C.E., Imam, Z., Ehrenberg, P.K. and Michael, N.L.				
TITLE	Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans				
JOURNAL	Genomics 80 (1), 86-95 (2002)				
MEDLINE	22074933				
PUBMED	12079287				
REFERENCE	2 (bases 1 to 5791)				
AUTHORS	Vijh, S., Dayhoff, D.E., Wang, C.E., Ehrenberg, P.K. and Michael, N.L.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S. Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD 20850, USA				
FEATURES	Location/Qualifiers				
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	/db_xref="taxon:9606"				
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	/clone="11A5, frag B"				
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gene	/gene="CCR3"				
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mRNA	/gene="CCR3"				
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	<4004..5562				
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	4015..5082				
CDS	/gene="CCR3"				
	/note="CCR3; G-protein coupled seven transmembrane spanning receptor; principle cell-surface receptor for eotaxin family of chemokines; expressed on eosinophils, CD4/Th2 and CD8 lymphocytes, monocytes, microglia, and dendritic cells"				
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	/product="CC chemokine receptor 3"				
	/protein_id="AAL85154.1"				
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polyA_signal	5542..5547				
polyA_site	/gene="CCR3"				
polyA_site	5562				
BASE COUNT	1624 a 1285 c 1160 g 1722 t				
ORIGIN					
Query Match	100.0%; Score 19; DB 9; Length 5791;				
Best Local Similarity	100.0%; Pred. No. 15;				

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
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Db 4119 CTGGGCCATCAGTCTCTG 4101

RESULT 36
AF224496S2/c 7010 bp DNA linear PRI 02-MAY-2001
LOCUS AF224496S2
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, exon 2 and partial cds.
ACCESSION AF224497
VERSION AF224497.1 GI:13924486
KEYWORDS
SEGMENT 2 of 2
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 7010)
AUTHORS Scotet,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2 cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 7010)
AUTHORS Scotet,E.J.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487 Grenzacherstrasse, Basel CH-4005, Switzerland
FEATURES
source 1. 7010
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order(AF224496.1:298..957,1..>7010)
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/number=2
6795..>7010
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BASE COUNT 2136 a 1420 c 1320 g 2129 t 5 others
ORIGIN

Query Match 100.0%; Score 19; DB 9; Length 7010;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
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Db 6899 CTGGGCCATCAGTCTCTG 6881

RESULT 37
AC138069/c 177334 bp DNA linear PRI 19-FEB-2003
LOCUS AC138069/c
DEFINITION Homo sapiens chromosome 3 clone RP13-54612, complete sequence.
ACCESSION AC138069
VERSION AC138069.3 GI:28416170
KEYWORDS HTG.

SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 177334)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 177334)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (10-JAN-2003) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE 4 (bases 1 to 177334)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-2003) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
On Feb 19, 2003 this sequence version replaced gi:27573398.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UMG
Web site: http://www.genome.washington.edu
Contact: uwgchgs@u.washington.edu
----- Project Information
Center project name: chr-3
Center clone name: RP13-54612 (bc0820)
----- Summary Statistics
Sequencing vector: plasmid; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 177210 bases at least Q40
Consensus quality: 177313 bases at least Q30
Consensus quality: 177334 bases at least Q20
Insert size: 177334; sum-of-contigs
Quality coverage: 9.3x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': RP11-793E15 (UMGC:bc0564) AC104439, 95469-bp overlap
3': U95626, 42710-bp overlap

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and

vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.

HindIII		BglII	
SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
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1239	1199	11125	10952
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449	<800	2290	2310
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510	<800	560	<800
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6511	6363	54	<800
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5296	5509	1159	1158
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10424	10027	4052	4034
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5046	5119	1846	1829
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1196	1199	8334	8273
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1397	1392	12882	12573
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2597	2624	448	<800
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1688	1674	12737	12573
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3800	3818	10300	10103
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2248	2269	6671	6656
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1074	1055	4052	4034
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7303	7718	1392	1386
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959	959	4253	4286
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551	<800	2791	2834
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1074	1055	2647	2682
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5688	5759	3423	3409
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5183	5363	73	<800
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3100	3093	499	<800
-----	-----	-----	-----
921	959	723	<800
-----	-----	-----	-----
4350	4244	2763	2834
-----	-----	-----	-----
4931	4857	6594	6656
-----	-----	-----	-----
3907	3818	4503	4468
-----	-----	-----	-----
8001	7718	5154	5136
-----	-----	-----	-----
3804	3818	4730	4713
-----	-----	-----	-----
2355	2376	13628	13324
-----	-----	-----	-----
862	868	166	<800
-----	-----	-----	-----
1711	1674	9554	9494
-----	-----	-----	-----
5672	5759	1398	1386

-----	3900	3818	1613	1641	1787	1756
-----	1905	1854	1479	1503	857	883
-----	7872	7718	1540	1503	1974	1945
-----	1174	1155	520	<800	1707	1631
-----	7015	7139	219	<800	3835	3756
-----	2852	2868	1571	1503	6586	6551
-----	221	<800	154	<800	178	<800
-----	1002	1055	5077	5136	2905	2871
-----	201	<800	2156	2190	2500	2501
-----	6717	6864	1075	1089	389	<800
-----	237	<800	162	<800	41	<800
-----	2737	2749	2752	2834	685	<800
-----	3448	3416	1647	1641	2598	2662
-----	3256	3238	7059	7056	248	<800
-----	5801	5759	1547	1503	2152	2210
-----	1512	1497	5163	5136	431	<800
-----	1398	1392	8679	8719	237	<800
-----	8413	8333	2033	2035	3380	3411
-----	6621	6614	886	892	5694	5744
-----	645	<800	-----	-----	3255	3265
-----	1026	1055	-----	-----	183	<800
-----	14333	14484	-----	-----	3128	3144
-----	-----	-----	-----	-----	10701	10790
-----	-----	-----	-----	-----	1321	1325

Query Match 100.0%; Score 19; DB 9; Length 177334;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
Db 88495 CTGGGCCATCAGTCTCTG 88477

RESULT 38
AC104439/c 197279 bp DNA linear PRI 20-JUN-2002
LOCUS AC104439 Homo sapiens chromosome 3 clone RP11-793E15, complete sequence.
DEFINITION AC104439 AC024739
ACCESSION AC104439.2 GI:21490240
VERSION AC104439.2 GI:21490240
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1 (bases 1 to 197279)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.

TITLE and Haugen,E.D.
JOURNAL Direct Submission
REFERENCE 2 (bases 1 to 197279)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 197279)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.

TITLE Direct Submission
JOURNAL Submitted (20-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On Jun 20, 2002 this sequence version replaced gi:17488621.

Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchgs@u.washington.edu
Drafting Center: WUGSC

Project Information
Center project name: chr-3
Center clone name: RP11-793E15 (bc0564)

Summary Statistics
Sequencing vector: unknown; 52% of reads
Sequencing vector: plasmid; 108752; 48% of reads
Chemistry: Dye-terminator ET; 94% of reads
Chemistry: Dye-terminator Big Dye; 6% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 197168 bases at least Q40
Consensus quality: 197255 bases at least Q30
Consensus quality: 197275 bases at least Q20
Insert size: 197279; sum-of-contigs
Quality coverage: 8.2x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': RP11-91E8 (UWGC:bc0216) AC026349
3': CTD-2563A18 (UWGC:bc0730)

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII BglII EcoRI
SeqDerMap FngPrnt SeqDerMap FngPrnt SeqDerMap FngPrnt

2687	2617	8949	8586	8696	8661
6382	6410	2067	2160	6	<800
512	<800	7846	7940	2742	2803
449	<800	3734	3895	5376	5324
2602	2763	1334	1301	1493	1478
2590	2617	2287	2309	823	835
8313	8291	1814	1918	1962	2002
1711	1683	691	<800	2900	2954
9821	9472	5477	5348	1484	1478
516	<800	305	<800	1005	995
8587	8291	25245	25541	1181	1171
7446	7581	3988	4121	18560	19002
2088	2075	1633	1598	3603	3579
2509	2617	631	<800	4943	5076
3519	3501	90	<800	3239	3241
26	<800	402	<800	953	995
925	933	3350	3490	1621	1615
98	<800	4577	4515	6827	6900
6409	6410	1229	1183	79	<800
1383	1376	4221	4331	16418	16263
16048	15829	3980	4121	3361	3241
1876	1877	2548	2497	872	881
4169	4068	674	<800	4220	4193
1674	1683	2332	2309	2848	2803
52	<800	11445	11045	2283	2318
5227	5082	5692	5632	3211	3241
15464	15829	1385	1414	4615	4632
14333	14296	608	<800	6823	6900
1026	1026	3930	3895	886	881
645	<800	1465	1414	2032	2002
6621	6410	2382	2497	8680	8661
8413	8291	747	<800	5163	5076
1401	1376	1951	2012	1547	1478
1512	1471	642	<800	7058	6900
5801	5644	21060	21003	1647	1615

3256	3278	3700	3666	2753	2803
3448	3501	1321	1301	162	<800
2738	2763	10705	10502	1078	1093
237	<800	3128	3317	2156	2173
6715	6823	183	<800	5077	5076
201	<800	3255	3490	154	<800
1002	1026	5693	5632	1571	1478
221	<800	3380	3317	219	<800
2854	2899	237	<800	520	<800
6998	7317	431	<800	1540	1478
1174	1145	2152	2160	1479	1478
7876	8291	249	<800	1613	1615
1911	1877	2599	2778	1399	1478
3899	3847	685	<800	9553	9383
5672	5644	41	<800	166	<800
1711	1683	388	<800	13615	13115
862	854	2500	2497	4731	4632
2368	2389	2889	2778	5159	5076
		178	<800	4503	4430
		6589	6728	6607	6900
		3836	3895	2766	2803

Query Match 100.0%; Score 19; DB 9; Length 197279;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
Db 190292 CTGGCCATCAGTCTCTG 190274

RESULT 39
HSA312688/c HSA312688 220965 bp DNA linear HTG 15-MAY-2002

LOCUS Homo sapiens chromosome 3 clone RP6-32g23 map 3p21.3, ***
DEFINITION SEQUENCING IN PROGRESS ***, 26 ordered pieces.

ACCESSION AJ312688.2 GI:13559235
VERSION AJ312688 HTG; HTGS_PHASE2.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Kiss, H., Yang, Y., Kiss, C., Andersson, K., Klein, G., Imreh, S. and

TITLE The transcriptional map of the common eliminated region 1 (C3CER1)
in 3p21.3

JOURNAL Eur. J. Hum. Genet. 10 (1), 52-61 (2002)

MEDLINE 21906202
PUBMED 11896456

REFERENCE 2 (bases 1 to 220965)

AUTHORS
TITLE
JOURNAL
COMMENT

Kiss, H.
Direct Submission
Submitted (01-APR-2001) Kiss H., Microbiology and Tumorbiology
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
SWEDEN

On Apr 5, 2001 this sequence version replaced gi:13548633.

The sequence is a consensus sequence of clone RP4-787c23 (1-140400
bp),

clone RP6-32g23 (31212-220965 bp), clone RP6-146e1 (partially,
1-6800 bp)

and clone RP6-188g11 (partially, 1-108303 bp). The sequencing
contigs are

in order and the gaps between them are represented by 100 Ns.

Contig 1:
1-11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp

Contig 4:
28448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp

Contig 7: 61679-97342 bp Contig 8: 97443-117655 bp Contig 9:
117756-118727 bp

Contig 10: 118828-121834 bp Contig 11: 121935-127855 bp Contig
12:
127956-129383 bp Contig 13: 129484-131747 bp Contig 14:
131848-132316 bp

Contig 15: 132417-134455 bp Contig 16: 134556-135527 bp Contig
17:
135628-189051 bp Contig 18: 189152-189476 bp Contig 19:
189577-191375 bp

Contig 20: 191476-201473 bp Contig 21: 201574-202307 bp Contig
22:
202408-204878 bp Contig 23: 204979-213531 bp Contig 24:
213632-218109 bp

Contig 25: 218210-219800 bp Contig 26: 219901-220965 bp.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 11731: contig of 11731 bp in length

* 11732 11831: gap of 100 bp

* 11832 26218: contig of 14387 bp in length

* 26219 26318: gap of 100 bp

* 26319 28347: contig of 2029 bp in length

* 28348 28447: gap of 100 bp

* 28448 42160: contig of 13713 bp in length

* 42161 42360: gap of 200 bp

* 42361 55059: contig of 12699 bp in length

* 55060 55159: gap of 100 bp

* 55160 61578: contig of 6419 bp in length

* 61579 97342: contig of 35664 bp in length

* 97343 97442: gap of 100 bp

* 97443 117655: contig of 20213 bp in length

* 117656 117755: gap of 100 bp

* 117756 118727: contig of 972 bp in length

* 118728 118827: gap of 100 bp

* 118828 121834: contig of 3007 bp in length

* 121835 121934: gap of 100 bp

* 121935 127855: contig of 5921 bp in length

* 127856 127955: gap of 100 bp

* 127956 129383: contig of 1428 bp in length

* 129384 129483: gap of 100 bp

* 129484 131747: contig of 2264 bp in length

* 131748 131847: gap of 100 bp

* 131848 132316: contig of 469 bp in length

* 132317 132416: gap of 100 bp

* 132417 134455: contig of 2039 bp in length

* 134456 134555: gap of 100 bp

* 134556 135527: contig of 972 bp in length

```
* 135528 135627: gap of 100 bp
* 135628 189051: contig of 53424 bp in length
* 189052 189151: gap of 100 bp
* 189152 189476: contig of 325 bp in length
* 189477 189576: gap of 100 bp
* 189577 191375: contig of 1799 bp in length
* 191376 191475: gap of 100 bp
* 191476 201473: contig of 9998 bp in length
* 201474 201573: gap of 100 bp
* 201574 202307: contig of 734 bp in length
* 202308 202407: gap of 100 bp
* 202408 204878: contig of 2471 bp in length
* 204879 204978: gap of 100 bp
* 204979 213531: contig of 8553 bp in length
* 213532 213631: gap of 100 bp
* 213632 218109: contig of 4478 bp in length
* 218110 218209: gap of 100 bp
* 218210 219800: contig of 1591 bp in length
* 219801 219900: gap of 100 bp
* 219901 220965: contig of 1065 bp in length.
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      /chromosome="3"
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ORIGIN
Query Match 100.0%; Score 19; DB 2; Length 220965;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTGCTCTG 19
Db 140368 CTGGGCCATCAGTGCTCTG 140350

RESULT 40
BC030031/c 1508 bp mRNA linear ROD 20-SEP-2002
LOCUS Mus musculus, lymphocyte antigen 108, clone MGC:41003
DEFINITION IMAGE:1225313, mRNA, complete cds.
ACCESSION BC030031
VERSION BC030031.1 GI:20988098
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1508)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: Soares Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
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Series: IRAK Plate: 66 Row: d Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 13507653.
Location/Qualifiers
  1. .1508
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    /mol_type="mRNA"
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    /clone_id="Soares_thymus_2NbMT"
    /lab_host="DH10B"
    /note="Vector: pTT73D-Pac"
    153. .1208
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TCQIHACVLKNGSOTVSVEWQATGNISLGPNTIFWDPNNGDQTVVCRKNAVSN
LSVSVSTQSLCKGVLINPWNVEMTTISIAVILLFVCWSIHVKRGSPLPTSQ
HPESQSTDPGSPGNTVYAQVTRMQEMKIPKPIKNDSMITIYSIVNHSREETVALTG
YNPITLKVNTLINYS"
BASE COUNT 482 a 342 c 321 g 363 t
ORIGIN
Query Match 91.6%; Score 17.4; DB 10; Length 1508;
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTGCTCTG 19
Db 1014 CTGGGCCATCAGTGCTCTG 996
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Search completed: January 13, 2004, 17:57:07
Job time : 747 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: January 13, 2004, 15:53:18 ; Search time 1192.5 seconds
(without alignments)
387.241 Million cell updates/sec

Title: US-09-719-737-18

Perfect score: 19
Sequence: 1 ctgggccatcagtcctctg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vrt: *
21: em_gss_fun: *
22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rtd: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gss1: *
29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	100.0	745	10	BG204024 RST23417
C 2	19	100.0	789	10	BG205056 RST24475
C 3	19	100.0	835	12	BI821796 BI821796
C 4	19	100.0	876	12	BI906283 BI906283

C 5	19	100.0	884	10	BG182330 RST1196 A
C 6	19	100.0	934	10	BG460984 RST43688
C 7	17.4	91.6	451	28	AQ571744 HS_5380 B
C 8	17.4	91.6	692	14	BY758727 BY758727
C 9	17.4	91.6	703	10	BB089480 BB089480
C 10	17.4	91.6	737	12	BG821437 BG821437
C 11	17.4	91.6	738	12	BG824723 BG824723
C 12	17.4	91.6	769	12	BG821578 BG821578
C 13	17.4	91.6	805	12	BI836792 BI836792
C 14	17.4	91.6	898	12	BG822063 BG822063
C 15	17.4	91.6	900	12	BG821494 BG821494
C 16	17.4	91.6	908	12	CNS034AE CNS034AE
C 17	17.4	91.6	1070	29	CNS034SN1 CNS034SN1
C 18	17.4	91.6	1579	10	BG327989 BG327989
C 19	17.4	91.6	1817	11	AK034665 AK034665
C 20	16.4	86.3	137	6	AL810567 AL810567
C 21	16.4	86.3	178	10	BF956881 BF956881
C 22	16.4	86.3	292	14	CA912316 CA912316
C 23	16.4	86.3	322	10	BF328982 BF328982
C 24	16.4	86.3	327	9	AW594895 AW594895
C 25	16.4	86.3	381	29	CC469335 CC469335
C 26	16.4	86.3	386	14	CB806515 CB806515
C 27	16.4	86.3	422	13	BY596515 BY596515
C 28	16.4	86.3	431	28	AZ786165 AZ786165
C 29	16.4	86.3	460	28	AQ706454 AQ706454
C 30	16.4	86.3	474	28	AZ813275 AZ813275
C 31	16.4	86.3	477	12	BI473885 BI473885
C 32	16.4	86.3	522	10	BG728994 BG728994
C 33	16.4	86.3	528	12	BG891847 BG891847
C 34	16.4	86.3	536	13	BQ616929 BQ616929
C 35	16.4	86.3	574	13	BQ074936 BQ074936
C 36	16.4	86.3	591	12	BI670955 BI670955
C 37	16.4	86.3	596	14	CA500347 CA500347
C 38	16.4	86.3	602	9	AI496684 AI496684
C 39	16.4	86.3	627	13	BQ074707 BQ074707
C 40	16.4	86.3	672	10	BE557791 BE557791
C 41	16.4	86.3	685	12	BM141543 BM141543
C 42	16.4	86.3	685	28	AQ995355 AQ995355
C 43	16.4	86.3	689	9	AF160693 AF160693
C 44	16.4	86.3	691	9	AW342617 AW342617
C 45	16.4	86.3	700	14	CD237190 CD237190

ALIGNMENTS

RESULT 1
LOCUS BG204024 745 bp mRNA linear EST 21-APR-2001
DEFINITION RST23417 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG204024
VERSION BG204024.1 GI:13725711
KEYWORDS EST.

SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens

REFERENCE
AUTHORS Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whitlington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
PUBMED 11329013

COMMENT
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596

Email: scai@athersys.com
High quality sequence stop: 447.

FEATURES

source

Location/Qualifiers
1. 745
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 159 a 207 c 170 g 209 t
ORIGIN

Query Match 100.0%; Score 19; DB 10; Length 745;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGGCCATCAGTCTCTG 19
Db 111 CTGGGCCATCAGTCTCTG 93

RESULT 2
BG205056/c 789 bp mRNA linear EST 21-APR-2001

LOCUS RST24475 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG205056
VERSION BG205056.1 GI:13726743

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 789)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,

Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,

Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith

,E., Veloso,N., Kliska,A., Hess,J., Cothren,K., Lo,K., Offenbacher

,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random

activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL 21227151
MEDLINE 11329013
PUBMED

COMMENT Contact: Scott J. Cain
Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596

Email: scai@athersys.com
High quality sequence stop: 521.

FEATURES
source Location/Qualifiers
1. 789

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 174 a 207 c 183 g 222 t 3 others

ORIGIN

Query Match 100.0%; Score 19; DB 10; Length 789;

Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGGCCATCAGTCTCTG 19
Db 120 CTGGGCCATCAGTCTCTG 102

RESULT 3

BI821796/c 835 bp mRNA linear EST 04-OCT-2001

LOCUS 603035872F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176960 5',
DEFINITION mRNA sequence.

ACCESSION BI821796
VERSION BI821796.1 GI:15933346

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 835)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: L1AM11440 row: p column: 17

High quality sequence start: 2
High quality sequence stop: 750.

FEATURES
source Location/Qualifiers
1. 835

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5176960"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"

/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."

BASE COUNT 206 a 217 c 210 g 202 t

ORIGIN

Query Match 100.0%; Score 19; DB 12; Length 835;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGGCCATCAGTCTCTG 19
Db 650 CTGGGCCATCAGTCTCTG 632

RESULT 4

BI906283/c 876 bp mRNA linear EST 16-OCT-2001

LOCUS 603063222F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212541 5',
DEFINITION mRNA sequence.

ACCESSION BI906283
VERSION BI906283.1 GI:16168946

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 876)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LLM11533 row: k column: 06
High quality sequence stop: 800.
Location/Qualifiers

FEATURES
source
1..876
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5212541"
/tissue_type="Leukocyte"
/lab_host="DH10B"
/clone_lib="NIH MGC 118"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH MGC Library."

BASE COUNT 202 a 232 c 193 g 249 t
ORIGIN

Query Match 100.0%; Score 19; DB 12; Length 876;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
|||||
Db 183 CTGGCCATCAGTCTCTG 165

RESULT 5
BG182330/c 884 bp mRNA linear EST 21-APR-2001
LOCUS RST1196 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
DEFINITION BG182330
ACCESSION BG182330
VERSION BG182330.1 GI:13704017
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 884)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Boozar,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
PUBMED 11329013
COMMENT Contact: Scott J. Cain

Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 529.
Location/Qualifiers

FEATURES
source
1..884
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression'
libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT 191 a 231 c 206 g 256 t
ORIGIN

Query Match 100.0%; Score 19; DB 10; Length 884;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
|||||
Db 121 CTGGCCATCAGTCTCTG 103

RESULT 6
BG460984/c 934 bp mRNA linear EST 21-APR-2001
LOCUS RST43688 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
DEFINITION BG460984
ACCESSION BG460984
VERSION BG460984.1 GI:13749490
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 934)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Boozar,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com.
Location/Qualifiers

FEATURES
source
1..934
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression'
libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT 200 a 188 c 237 g 282 t 27 others

ORIGIN

Query Match 100.0%; Score 19; DB 10; Length 934;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGGGCCATCAGTCTCTG 19
|||||
Db 179 CTGGGCCATCAGTCTCTG 161

RESULT 7
AQ571744
LOCUS

DEFINITION HS_5380_B2_H12_SP6E RPCI-11 Human Male BAC library Homo sapiens
genomic clone Plate=956 Col=24 Row=P, genomic survey sequence.

ACCESSION AQ571744
VERSION AQ571744.1 GI:4964898
KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 451)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

JOURNAL
MEDLINE
PUBMED

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 956 row: P column: 24
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 451.

FEATURES

source

1..451
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=956 Col=24 Row=P"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC library"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"

BASE COUNT 101 a 132 c 110 g 108 t
ORIGIN

Query Match 91.6%; Score 17.4; DB 28; Length 451;
Best Local Similarity 94.7%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CTGGGCCATCAGTCTCTG 19
|||||
Db 174 CTGGGCCATCAGTCTCTG 192

RESULT 8

BY758727/c

LOCUS

DEFINITION

BY758727 RIKEN full-length enriched, CRL-1722 L5178Y-R Mus musculus
cDNA clone I730064J16 3', mRNA sequence.

ACCESSION

BY758727

VERSION

BY758727.1

KEYWORDS

EST.

SOURCE

Mus musculus

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.,
Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chochia,C., Corbani
L.B., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.,
Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
Jarvis,E.D., Kanai,A., Kawai,H., Kawasawa,Y., Kedzierski,R.M.,
King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons
P.A., Maglott,D.R., Maltas,L., Marchionni,L., McKenzie,L., Miki
H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G.,
Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D.,
Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring
B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou
M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale
R.D., Tomita,M., Verrardo,R., Wagner,L., Wahlestedt,C., Wang,Y.,
Watanabe,Y., Wells,C., Wilming,L.G., Wyszewski-Boris,A., Yanagisawa
M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A.,
Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Kono,H., Nakamura
M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii
Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata
K., Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander
E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Kono
H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Osato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Location/Qualifiers

1. 692
/organism="Mus musculus"
/mol_type="mRNA"
/strain="DBA/2"
/db_xref="taxon:10090"
/clone="I730064J16"
/cell_line="CRL-1722 L5178Y-R"
/clone_lib="RIKEN full-length enriched, CRL-1722 L5178Y-R"

BASE COUNT 214 a 149 c 152 g 174 t 3 others

ORIGIN

Query Match 91.6%; Score 17.4; DB 14; Length 692;
Best Local Similarity 94.7%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGCATCAGTCTCTG 19

Db 230 CTGGGCATCTGTCTCTG 212

RESULT 9
LOCUS BB089480/c 703 bp mRNA linear EST 18-OCT-2001
DEFINITION BB089480 RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck Mus musculus cDNA clone 9430022H21 3', mRNA sequence.

ACCESSION BB089480 GI:16261010

VERSION BB089480.2

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 703)

Akakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M., and Hayashizaki,Y.

RIKEN Mouse ESTs (Akakawa,T., et al. 2001)

Unpublished

On Jun 21, 2000 this sequence version replaced gi:8655274.

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa

,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and

Hayashizaki,Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

further details.

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

FEATURES

SOURCE

Location/Qualifiers

1. 703
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="9430022H21"
/tissue_type="embryonic body between diaphragm region and neck"

/dev_stage="12 days embryo"

/lab_host="DH10B"

/clone_lib="RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was

primed with a primer [5'

GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was

prepared by using trehalose thermo-activated reverse

transcriptase and subsequently enriched for full-length by

cap-trapper. cDNA went through one round of normalization

to Rot = 20.0 and subtraction to Rot = 370.0. Second

strand cDNA was prepared with the primer adapter of

sequence [5' GAGAGAGAGATTCTCGAGTTAATTAATTAATCCCCCCCC

3']. cDNA was cleaved with XhoI and BamHI."

BASE COUNT 244 a 162 c 133 g 161 t 3 others

ORIGIN

Query Match 91.6%; Score 17.4; DB 10; Length 703;

Best Local Similarity 94.7%; Pred. No. 1.1e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGCATCAGTCTCTG 19

Db 358 CTGGGCATCAGTCTCTG 340

RESULT 10
LOCUS BG821437/c 737 bp mRNA linear EST 22-MAY-2001
DEFINITION 602724894F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4864654 5', mRNA sequence.

ACCESSION BG821437 GI:14169024

VERSION BG821437.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov

Plate: LLCM1728 row: k column: 23
High quality sequence stop: 734.

FEATURES

source

1. 737

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4864654"

/tissue_type="adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_15"

/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 170 a 214 c 223 g 130 t
ORIGIN

Query Match

Best Local Similarity 91.6%; Score 17.4; DB 12; Length 737;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGGGCCATCAGTGTCTTG 19
|||||
Db 45 CTGGGCCATGAGTGTCTTG 27

RESULT 11

BG824723 738 bp mRNA linear EST 22-MAY-2001

LOCUS 602728705F1 NIH_MGC_15 Homo sapiens CDNA clone IMAGE:4868064 5',

DEFINITION mRNA sequence.

ACCESSION BG824723 GI:14172310

VERSION BG824723

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 738)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: NIH Intramural Sequencing Center

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: LLCM1737 row: j column: 01

High quality sequence stop: 728.

FEATURES

source

1. 738

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4868064"

/tissue_type="adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_15"

/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 168 a 211 c 229 g 130 t
ORIGIN

Query Match

Best Local Similarity 91.6%; Score 17.4; DB 12; Length 738;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGGGCCATCAGTGTCTTG 19
|||||
Db 45 CTGGGCCATGAGTGTCTTG 27

RESULT 12

BG821578 769 bp mRNA linear EST 22-MAY-2001

LOCUS 602725172F1 NIH_MGC_15 Homo sapiens CDNA clone IMAGE:4864768 5',

DEFINITION mRNA sequence.

ACCESSION BG821578 GI:14169165

VERSION BG821578

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 769)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: NIH Intramural Sequencing Center

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: LLCM1728 row: p column: 17

High quality sequence stop: 692.

FEATURES

source

1. 769

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4864768"

/tissue_type="adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_15"

/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 182 a 217 c 235 g 135 t
ORIGIN

Query Match

Best Local Similarity 91.6%; Score 17.4; DB 12; Length 769;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
|||||
Db 45 CTGGGCCATCAGTCTCTG 27

RESULT 13
BI836792 805 bp mRNA linear EST 04-OCT-2001
LOCUS 603084870F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5224073 5',
DEFINITION mRNA sequence.
ACCESSION BI836792
VERSION BI836792.1 GI:15948342
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 805)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11563 row: k column: 18
High quality sequence start: 2
High quality sequence stop: 635.
Location/Qualifiers

FEATURES
source
1..805
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5224073"
/lab_host="DH10B"
/clone_lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT 190 a 219 c 245 g 151 t
ORIGIN

Query Match 91.6%; Score 17.4; DB 12; Length 805;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
|||||
Db 527 CTGGGCCATCAGCTCTG 545

RESULT 14
BG822063 898 bp mRNA linear EST 22-MAY-2001
LOCUS 602726178F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4865803 5',
DEFINITION mRNA sequence.
ACCESSION BG822063
VERSION BG822063.1 GI:14169650
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1731 row: k column: 20
High quality sequence stop: 821.
Location/Qualifiers

FEATURES
source
1..898
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4865803"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_15"
/note="Organ: colon; Vector: POTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit.
(Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 200 a 258 c 278 g 162 t
ORIGIN

Query Match 91.6%; Score 17.4; DB 12; Length 898;
Best Local Similarity 94.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
|||||
Db 45 CTGGGCCATCAGTCTCTG 27

RESULT 15
BG821494 900 bp mRNA linear EST 22-MAY-2001
LOCUS 602725068F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4864577 5',
DEFINITION mRNA sequence.
ACCESSION BG821494
VERSION BG821494.1 GI:14169081
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 900)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1728 row: h column: 18
High quality sequence stop: 808.
Location/Qualifiers

FEATURES
location/Qualifiers

```
source
1. .900
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4864577"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 15"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT      211 a      258 c      273 g      158 t
ORIGIN

Query Match      91.6%; Score 17.4; DB 12; Length 900;
Best Local Similarity 94.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGGGCCATCAGTGTCTG 19
        ||||| ||||| ||||| |||||
Db      45 CTGGGCCATGAGTGTCTG 27

RESULT 16
CNS03A4E      908 bp      DNA      linear      GSS 01-SEP-2000
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
008L02 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL234743      GI:7893878
AL234743.1    GI:7893878
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE
1 Roest Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
  Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
  Saurin,W. and Weissenbach,J.
  Estimate of human gene number provided by genome-wide analysis
  using Tetraodon nigroviridis DNA sequence
  Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL
MEDLINE
PUBMED
20296633
10835645

REFERENCE
2 Roest Crolius,H., Jallion,O., Dasilva,C., Ozouf-Costaz,C.,
  Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
  Saurin,W., Bernot,A. and Weissenbach,J.
  Characterization and repeat analysis of the compact genome of the
  freshwater pufferfish Tetraodon nigroviridis
  Genome Res. 10 (7), 939-949 (2000)

JOURNAL
MEDLINE
PUBMED
20359837
10899143

REFERENCE
3 (bases 1 to 908)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source
1. .908
Location/Qualifiers
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/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="008L02"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG008DF01SP1-end :
PUC-Ori"

BASE COUNT      229 a      255 c      195 g      229 t
ORIGIN

Query Match      91.6%; Score 17.4; DB 29; Length 908;
Best Local Similarity 94.7%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGGGCCATCAGTGTCTG 19
        ||||| ||||| ||||| |||||
Db      877 CTGACCATCAGTGTCTG 895
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```
RESULT 17
CNS03SN1      1070 bp      DNA      linear      GSS 01-SEP-2000
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
054A19 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL258742      GI:7979754
AL258742.1    GI:7979754
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE
1 Roest Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
  Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
  Saurin,W. and Weissenbach,J.
  Estimate of human gene number provided by genome-wide analysis
  using Tetraodon nigroviridis DNA sequence
  Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL
MEDLINE
PUBMED
20296633
10835645

REFERENCE
2 Roest Crolius,H., Jallion,O., Dasilva,C., Ozouf-Costaz,C.,
  Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
  Saurin,W., Bernot,A. and Weissenbach,J.
  Characterization and repeat analysis of the compact genome of the
  freshwater pufferfish Tetraodon nigroviridis
  Genome Res. 10 (7), 939-949 (2000)

JOURNAL
MEDLINE
PUBMED
20359837
10899143

REFERENCE
3 (bases 1 to 1070)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source
1. .1070
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="054A19"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG054AA10LP1-end : T7"

BASE COUNT      244 a      270 c      279 g      270 t
ORIGIN
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Query Match 91.6%; Score 17.4; DB 29; Length 1070;
Best Local Similarity 94.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTGTCTG 19
|||||
Db 225 CTGGGCCATCAGTGTCTG 243

RESULT 18
BG327989/c 1579 bp mRNA linear EST 27-FEB-2001
LOCUS DEFINITION 602427610F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:454689 5',
RNA sequence.
ACCESSION BG327989
VERSION BG327989.1 GI:13134427
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1579)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM1234 row: d column: 04
High quality sequence stop: 197.
Location/Qualifiers
1.1579
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4546899"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH MGC 15"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 475 a 773 c 218 g 113 t
ORIGIN

Query Match 91.6%; Score 17.4; DB 10; Length 1579;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTGTCTG 19
|||||
Db 47 CTGGGCCATCAGTGTCTG 29

RESULT 19
AK034665/c 1817 bp mRNA linear HTC 05-DEC-2002
LOCUS DEFINITION Mus musculus 12 days embryo embryonic body between diaphragm region
and neck cDNA, RIKEN full-length enriched library, clone:9430022H21
product:unknown EST, full insert sequence.
ACCESSION AK034665
VERSION AK034665.1 GI:26084119

KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci P. and Hayashizaki Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE 2
AUTHORS Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Itoh M., Konno H., Okazaki Y., Muramatsu M. and Hayashizaki Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

REFERENCE 3
AUTHORS Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A. and Hayashizaki Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861

REFERENCE 4
AUTHORS Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konno S., Yamada S.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G.,
Quackenbush J., Schriml L.M., Staahl F., Suzuki R., Tomita M.,
Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H.,
Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N.,
Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C.,
Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D.,
Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P.,
Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P.,
Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H.,
Sato K., Schonbach C., Seya T., Shibata Y., Storch K.F., Suzuki H.,
Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.
and Hayashizaki Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851

REFERENCE 5
AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6
AUTHORS Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M.,
Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N.,
Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N.,
Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T.,
Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S.,


```
/clone_lib="NN0233"
/notes="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      45 a      37 c      40 g      56 t
ORIGIN
Query Match      86.3%; Score 16.4; DB 10; Length 178;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      2 TGGGCCATCAGTGCTCTG 19
      |||||
Db      10 TGTGCCATCAGTGCTCTG 27

RESULT 22
CA912316      292 bp      mRNA      linear      EST 27-DEC-2002
LOCUS      PCS03177 scarlet Runner Bean Suspensor Region Triplex2 Phaseolus
DEFINITION      coccineus cDNA 3' similar to putative protein; protein id:
      At3g57150, mRNA sequence.
ACCESSION      CA912316
VERSION      CA912316.1 GI:27399308
KEYWORDS      EST.
SOURCE      Phaseolus coccineus
ORGANISM      Phaseolus coccineus
      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
      ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
      phaseolus.
      1 (bases 1 to 292)
REFERENCE      Bui,A.Q., Le,B.H., Weterings,K., Bi,Y.-P., Choi,J.-S., McElroy,K.E.
AUTHORS      , Choi,P.S., Harada,J.J., Fischer,R.L. and Goldberg,R.B.
TITLE      Gene Activity in Different Regions of a Post-Fertilization Plant
      Embryo by EST Analysis
JOURNAL      Unpublished
COMMENT      Contact: Goldberg, R.B.
      Department of Molecular, Cell, & Developmental Biology
      University of California, Los Angeles
      621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA
      Tel: 310 825 3270
      Fax: 310 825 8201
      Email: bobg@ucla.edu
      Seg primer: 5' Triplex
      POLYA=No.
FEATURES
      source
      1..292
      Location/Qualifiers
      /organism="Phaseolus coccineus"
      /mol_type="mRNA"
      /cultivar="Hammond's Dwarf Scarlet"
      /db_xref="taxon:3886"
      /dev_stage="6-days post-pollination"
      /clone_lib="Scarlet Runner Bean Suspensor Region Triplex2"
      /note="Organ: Suspensor Region of Globular-Stage Embryos;
      Vector: Triplex2; Site_1: SfiIA; Site_2: SfiIB; Suspensor
      regions were micro-dissected from globular-stage embryos
      six days after pollination from greenhouse-grown plants
      [Weterings et al., Plant Cell 13, 2409-2425 (2001)].
      Double-stranded cDNA was synthesized from suspensor mRNA
      using the SMART cDNA Library Construction Kit according to
      the manufacturer (Clontech). The suspensor cDNA fragments
      were directionally ligated into the SfiI restriction site
      of the lambda Triplex2 vector (Clontech), and the
      recombinant cDNAs were transformed into E. coli XL1-Blue
      cells (Clontech). Suspensor cDNA plasmids used for
      directional sequencing were obtained by in vivo excision
      from the lambda Triplex2 recombinants in E. coli BM25.8
      cells (Clontech)."
```

```
BASE COUNT      95 a      44 c      97 g      56 t
ORIGIN
Query Match      86.3%; Score 16.4; DB 14; Length 292;
Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 CTGGCCATCAGTGCTCT 18
      |||||
Db      172 CTGGGCTATCAGTGCTCT 155

RESULT 23
BF328982      322 bp      mRNA      linear      EST 22-NOV-2000
LOCUS      MR4-BN0238-010800-001-e03 BN0238 Homo sapiens cDNA, mRNA sequence.
DEFINITION      BF328982
ACCESSION      BF328982
VERSION      BF328982.1 GI:11299730
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 322)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
      Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
      Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
      Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
      ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
      Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
      sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
      Laboratory of Cancer Genetics
      Ludwig Institute for Cancer Research
      Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp,
      Brazil
      Tel: +55-11-2704922
      Fax: +55-11-2707001
      Email: asimpson@ludwig.org.br
      This sequence was derived from the FAPESP/LICR Human Cancer Genome
      Project. This entry can be seen in the following URL
      (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-BN0238-
      010800-001-e03&t3=2000-08-01&t4=1)
      Seg primer: puc 18 forward
      High quality sequence start: 28
      High quality sequence stop: 322.
      High quality sequence
FEATURES
      source
      1..322
      Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /dev_stage="Adult"
      /clone_lib="BN0238"
      /note="Organ: breast normal; Vector: puc18; Site_1: SmaI;
      Site_2: SmaI; A mini-library was made by cloning products
      derived from ORESTES PCR (U.S. Letters Patent application
      No. 196,716 - Ludwig Institute for Cancer Research)
      profiles into the pUC 18 vector. Reverse transcription of
      tissue mRNA and cDNA amplification were performed under
      low stringency conditions."
BASE COUNT      113 a      64 c      59 g      86 t
ORIGIN
Query Match      86.3%; Score 16.4; DB 10; Length 322;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      2 TGGGCCATCAGTGCTCTG 19
      |||||
```

Db 224 TGGGCCATGAGTCTCTG 207

RESULT 24
AM594895/c
LOCUS
DEFINITION AM594895 327 bp mRNA linear EST 22-MAR-2000
fk26a06.y1 zebrafish fin day1 regeneration Danio rerio cDNA 5'
similar to SW:IAIP_CHICK Q90660 INHIBITOR OF APOPTOSIS PROTEIN ;,
mRNA sequence.

ACCESSION AM594895
VERSION AM594895.1 GI:7282153
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 327)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,B.,
Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.
Washu Zebrafish EST Project 1998
Unpublished
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@watson.wustl.edu
cDNA Library Preparation: Raymond Lee. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
ResourcenZentrumPrimateBank, Berlin, Germany (web address:
www.rzpd.de)
Seq primer: T3 ET from Amersham
High quality sequence stop: 316.
Location/Qualifiers
1. 327
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/sex="mixed male and female"
/tissue_type="1 day fin regenerates"
/lab_host="E. coli XL0LR"
/clone_lib="zebrafish fin day1 regeneration"
/note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; 1st
strand cDNA primed with (GA)TACTAGTCTGAG(T)18, followed
by second strand synthesis, and ligated to 5' adapter (5'
)-aatcgscagcag-3', 3'-gccgtgctc-5'. cDNA was cloned
directionally (EcoRI/XhoI) into Stratagene Zap express
lambda phage arms. Mass invivo excision done to obtain
inserts in pBK-CMV phagemid."

BASE COUNT 100 a 67 c 80 g 80 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 9; Length 327;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGCCATGAGTCTCT 18
|||||
Db 70 CTGGGCCATGAGTCTCT 53

RESULT 25
CC469335/c
LOCUS CC469335 381 bp DNA linear GSS 12-JUN-2003

DEFINITION CH240_141P20.TV CHORI-240 Bos taurus genomic clone CH240_141P20,
genomic survey sequence.

ACCESSION CC469335
VERSION CC469335.1 GI:31655567
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 381)
Costa,J.N., Mota,M. and Caetano,A.R.
Brazil's Contribution to End-Sequencing the Bovine BAC Library
CHORI-240
Unpublished
Other_GSSs: CH240_141P20.TJ
Contact: Caetano AR
Department of Biotechnology
Embrapa Recursos Geneticos e Biotecnologia
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.
02372, 70770-900 Brasil
Tel: 55 61 448 4778
Fax: 55 61 340 3658
Email: acetano@cenargen.embrapa.br
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). Bases shown have phred
quality value equal to or higher then 20. Bases with quality value
below 20 were masked with 'N'. For BAC library availability, please
contact Pieter de Jong (pdejong@mail.cho.org). Clones may be
purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia
with financing from Conselho Nacional de Desenvolvimento Cientifico
e Tecnolico (CNPq), Brazil.
Plate: 141 row: P column: 20
Seq primer: T7
Class: BAC ends
High quality sequence stop: 381.
Location/Qualifiers
1. 381
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_141P20"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull LI Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

BASE COUNT 99 a 78 c 82 g 61 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 29; Length 381;
Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGCCATGAGTCTCT 18
|||||
Db 219 CTGGTCCATGAGTCTCT 202

RESULT 26
CB806515/c
LOCUS CB806515 386 bp mRNA linear EST 16-MAY-2003
DEFINITION AMGNNUC:NRDGI-00115-A10-A nrdg1 (10855) Rattus norvegicus cDNA
clone nrdg1-00115-a10 5', mRNA sequence.
ACCESSION CB806515
VERSION CB806515.1 GI:29924649
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)

```

ORGANISM      Rattus norvegicus
               Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
               Rattus.
REFERENCE      1 (bases 1 to 386)
AUTHORS        Amgen EST Program.
TITLE          Amgen Rat EST Program
JOURNAL        Unpublished
COMMENT        Contact: Dan Fitzpatrick
               Amgen, Inc
               One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
               Tel: 805 447-4881
               Plate: 00115 row: a column: 10.
               Location/Qualifiers
FEATURES       source
               1..386
               /organism="Rattus norvegicus"
               /mol_type="mRNA"
               /db_xref="taxon:10116"
               /clone="nr01-00115-a10"
               /tissue_type="Dorsal Root Ganglia"
               /clone_lib="nr01 (10855)"
               /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat
               dorsal root ganglia"
BASE COUNT     128 a      61 c      82 g      115 t
ORIGIN
Query Match    86.3%; Score 16.4; DB 14; Length 386;
Best Local Similarity 94.4%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGGGCCATCAGTGCTCT 18
        ||||| ||||| ||||| |||||
Db      34 CTGGGCCATCAGTGCTCT 17

RESULT 27
BY596515/c     422 bp      mRNA      linear      EST 15-DEC-2002
LOCUS          BY596515 RIKEN full-length enriched, adult inner ear Mus musculus
DEFINITION     CDNA clone F930050L08 3', mRNA sequence.
ACCESSION      BY596515
VERSION        BY596515.1 GI:26931697
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 422)
AUTHORS        Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
               Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.,
               Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
               Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
               Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
               Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chotia,C., Corbani
               ,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
               ,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.,
               Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
               Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
               King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons
               ,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki
               ,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G.,
               Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D.,
               Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring
               ,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempke,C.A., Setou
               ,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale
               ,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y.,
               Watanabe,Y., Wells,C., Wilming,L.G., Wyszynski-Boris,A., Yanagisawa
               ,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A.,
               Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura
               ,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
               Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii
               ,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata
               ,K., Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander

```

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TITLE          'E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
JOURNAL        Analysis of the mouse transcriptome based on functional annotation
MEDLINE        of 60,770 full-length cDNAs
PUBMED         Nature 420, 563-573 (2002)
22354683
12466851
COMMENT        Contact: Yoshihide Hayashizaki
               Laboratory for Genome Exploration Research Group, RIKEN Genomic
               Sciences Center(GSC), Yokohama Institute
               The Institute of Physical and Chemical Research (RIKEN)
               1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
               Tel: 81-45-503-9222
               Fax: 81-45-503-9216
               Email: genome-res@sc.riken.go.jp,
               URL:http://genome.gsc.riken.go.jp/
               Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
               ,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
               Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
               Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
               ,M., Waki,K., Wataniki,A., Muramatsu,M. and Hayashizaki,Y. Direct
               Submission
               Computational Analysis of Full-length Mouse cDNAs Compared with
               Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
               Normalization and subtraction of cap-trapper-selected cDNAs to
               prepare full-length cDNA libraries for rapid discovery of new
               genes. Genome Res. 10 (10), 1617-1630 (2000)
               RIKEN integrated sequence analysis (RISA) system--384-format
               sequencing pipeline with 384 multicapillary sequencer. Genome Res.
               10 (11), 1757-1771 (2000)
               Computer-based methods for the mouse full-length cDNA
               encyclopedia: real-time sequence clustering for construction of a
               nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
               cDNA library was prepared and sequenced in Mouse Genome
               Encyclopedia Project of Genome Exploration Research Group in Riken
               Genomic Sciences Center and Genome Science Laboratory in RIKEN.
               Division of Experimental Animal Research in Riken contributed to
               prepare mouse tissues.
               Tissues were provided by Kirk W. Beisel ( Boys Town National
               Research Hospital 555 North 30th Street Omaha,NE 68131 USA ) whose
               assistance we gratefully acknowledge.
               Please visit our web site (http://genome.gsc.riken.go.jp) for
               further details.
FEATURES       Location/Qualifiers
SOURCE         1..422
               /organism="Mus musculus"
               /mol_type="mRNA"
               /strain="C57Bl/6J"
               /db_xref="taxon:10090"
               /clone="F930050L08"
               /tissue_type="inner ear"
               /dev_stage="adult"
               /clone_lib="RIKEN full-length enriched, adult inner ear"
BASE COUNT     107 a      90 c      118 g      107 t
ORIGIN
Query Match    86.3%; Score 16.4; DB 13; Length 422;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TGGGCCATCAGTGCTTG 19
        ||||| ||||| ||||| |||||
Db      173 TGGGCCATCAGTGATCTG 156

RESULT 28
AZ786165/c     431 bp      DNA      linear      GSS 16-FEB-2001
LOCUS          AZ786165 2M0031F02R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION     clone UUCG2M0031F02 R, genomic survey sequence.
ACCESSION      AZ786165
VERSION        AZ786165.1 GI:12923652
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)

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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 431)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: F column: 02
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 431.
Location/Qualifiers
1. 431
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UTGC2M0031F02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 112 a 95 c 111 g 113 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 28; Length 431;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGCCATCATGCTCT 18
|||
Db 384 CTGGCCATCATGCTCT 367

RESULT 29
AQ706454/c 460 bp DNA linear GSS 07-JUL-1999
LOCUS
DEFINITION HS_5554_A1 G06 SP6B RPCI-11 Human Male BAC library Homo sapiens genomic clone Plate=1130 Col=11 Row=M, genomic survey sequence.
ACCESSION AQ706454
VERSION AQ706454.1 GI:5415880
KEYWORDS GSS.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 460)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1130 row: M column: 11
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 460.
Location/Qualifiers
1. 460
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=1130 Col=11 Row=M"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC library"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

BASE COUNT 166 a 71 c 123 g 97 t 3 others
ORIGIN

Query Match 86.3%; Score 16.4; DB 28; Length 460;
Best Local Similarity 94.4%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGGCCATCATGCTCTG 19
|||
Db 412 TTGGCCATCATGCTCTG 395

RESULT 30
AZ813275 474 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION 2M0080A05R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC2M0080A05 R, genomic survey sequence.
ACCESSION AZ813275
VERSION AZ813275.1 GI:12983183
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 474)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT

plasmid inserts
unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: A column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 474.

FEATURES
source

1.477
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0080A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

78 a 143 c 136 g 117 t

Query Match

Best Local Similarity 86.3%; Score 16.4; DB 28; Length 474;
Matches 17; Conservativity 94.4%; Pred. No. 2.5e+03;
Matches 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGGGCATCAGTCTCT 18
Db 337 CTGGCCTTCAGTCTCT 354

RESULT 31
BI473885

LOCUS BI473885 477 bp mRNA linear EST 27-AUG-2001
DEFINITION fp48b06.y3 zebrafish gridded kidney Danio rerio cDNA clone
IMAGE:4759643 5' similar to SW:IAP_CHICK Q90660 INHIBITOR OF

APOPTOSIS PROTEIN ;, mRNA sequence.
AP0TOSIS PROTEIN ;, mRNA sequence.

ACCESSION BI473885
VERSION BI473885.1
KEYWORDS GI:15302437
SOURCE EST.
ORGANISM Danio rerio (zebrafish)

REFERENCE 1 (bases 1 to 477)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood

TITLE
JOURNAL
COMMENT

'K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.
Washu Zebrafish EST Project 1998
Unpublished
Other ESTs: fp48b06.x3

Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
CDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:
www.genomesystems.com) (email contact: info@genomesystems.com) and
Research Genetics, Huntsville, Alabama (web address: www.resgen.com
) (email contact: info@resgen.com) and
Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:
www.rzpd.de)
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 294.

FEATURES
source

1.477
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:4759643"
/sex="mixed"
/tissue_type="kidney pooled from 300 wild type adults"
/lab_host="XL0LR"
/clone_lib="zebrafish gridded kidney"
/note="Organ: kidney; Vector: PBK-CMV; Site 1: EcoRI;
Site 2: XhoI; Oligo dT cDNA library constructed from mRNA
pooled from pooled kidney tissue from 300 adult
zebrafish."

BASE COUNT
ORIGIN

114 a 109 c 96 g 158 t

Query Match

Best Local Similarity 86.3%; Score 16.4; DB 12; Length 477;
Matches 17; Conservativity 94.4%; Pred. No. 2.5e+03;
Matches 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGGGCATCAGTCTCT 18
Db 289 CTGGCCTTCAGTCTCT 306

RESULT 32
BG728994

LOCUS BG728994 522 bp mRNA linear EST 09-MAY-2001
DEFINITION fp06g01.x1 zebrafish gridded kidney Danio rerio cDNA clone
IMAGE:4728769 3' similar to SW:IAP_CHICK Q90660 INHIBITOR OF

APOPTOSIS PROTEIN ;, mRNA sequence.
AP0TOSIS PROTEIN ;, mRNA sequence.

ACCESSION BG728994
VERSION BG728994.1
KEYWORDS GI:14014069
SOURCE EST.
ORGANISM Danio rerio (zebrafish)

REFERENCE 1 (bases 1 to 522)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.

TITLE Washu Zebrafish EST Project 1998
JOURNAL Unpublished
COMMENT Contact: Stephen L. Johnson

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
CDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:
www.genomesystems.com) (email contact: info@genomesystems.com) and
Research Genetics, Huntsville, Alabama (web address: www.resgen.com
) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
www.rzpd.de)
Seq primer: T7 from Gibco
High quality sequence stop: 361.
Location/Qualifiers
1. 522
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:4728769"
/sex="mixed"
/tissue_type="kidney pooled from 300 wild type adults"
/lab_host="XLOLR"
/clone_lib="zebrafish gridded kidney"
/note="Organ: kidney; Vector: PBK-CMV; Site 1: EcorI;
Site 2: XhoI; Oligo dt cDNA library constructed from mRNA
pooled from pooled kidney tissue from 300 adult
zebrafish."

BASE COUNT 133 a 123 c 106 g 160 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 10; Length 522;
Best Local Similarity 94.4%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGGGCCATCAGTCTCT 18
|||||
Db 254 CTGGGCCATCAGTCTCT 271

RESULT 33
BG891847 528 bp mRNA linear EST 04-JUN-2001
LOCUS
DEFINITION
IMAGE:4759752 3', similar to SW:IAF_CHICK Q90660 INHIBITOR OF
APOPTOSIS PROTEIN ;, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 528)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.
Washu Zebrafish EST Project 1998
Unpublished
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:

www.genomesystems.com) (email contact: info@genomesystems.com) and
Research Genetics, Huntsville, Alabama (web address: www.resgen.com
) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
www.rzpd.de)
High quality sequence stop: 374.
Location/Qualifiers
1. 528
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:4759752"
/sex="mixed"
/tissue_type="kidney pooled from 300 wild type adults"
/lab_host="XLOLR"
/clone_lib="zebrafish gridded kidney"
/note="Organ: kidney; Vector: PBK-CMV; Site 1: EcorI;
Site 2: XhoI; Oligo dt cDNA library constructed from mRNA
pooled from pooled kidney tissue from 300 adult
zebrafish."

BASE COUNT 132 a 126 c 108 g 162 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 12; Length 528;
Best Local Similarity 94.4%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTGGGCCATCAGTCTCT 18
|||||
Db 253 CTGGGCCATCAGTCTCT 270

RESULT 34
B0616929 536 bp mRNA linear EST 26-JUN-2002
LOCUS
DEFINITION
IMAGE:6034059 3', similar to SW:IAF2_HUMAN Q13490 INHIBITOR OF
APOPTOSIS PROTEIN 2 ;, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 536)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.
Washu Zebrafish EST Project 1998
Unpublished
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution information can be found through the I.M.A.G.E.
Consortium/BLN, send email to: info@image.llnl.gov
Seq primer: T7 from Gibco.
Location/Qualifiers
1. 536
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:6034059"
/sex="male"


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/tissue_type="whole body"
/dev_stage="adult"
/lab_host="DH10B (phage resistant)"
/clone_lib="Sugano SJD adult male"
/note="Vector: pME18S-FL3; Site_1: DraIII (CACCATGTG);
Site_2: DraIII (CACTGTGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTCTTTTCTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TTGTGGCCTTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed and donated by Dr. Sumio
Sugano (University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTCTMAAGCTGCG and 3' end primer
CGACCTGCAGCTCGAGCACA."
```

BASE COUNT 132 a 126 c 107 g 171 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 13; Length 536;
Best Local Similarity 94.4%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCT 18
|||||
Db 264 CTGGGCCATCAGTCTCT 281

RESULT 35 574 bp mRNA linear EST 02-APR-2002
BQ074936/c LOCUS
DEFINITION fz24f09.y1 Gong zebrafish testis Danio rerio cDNA 5' similar to
SW:IAIP2_HUMAN Q13490 INHIBITOR OF APOPTOSIS PROTEIN 2 ;, mRNA
sequence.
ACCESSION BQ074936
VERSION BQ074936.1 GI:19903973
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 574)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.
TITLE Washu Zebrafish EST Project 1998
JOURNAL Unpublished
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
The library was constructed by Dr. Z. Gong. DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis. Please
contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119260).
Seq primer: T3 ET from Amersham
High quality sequence stop: 424.
location/Qualifiers
1..574
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/sex="male"
/dev_stage="4-5 month"
/lab_host="DH10B (phage-resistant)"

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/clone_lib="Gong zebrafish testis"  
/note="Organ: testis (pooled); Vector: pBluescript SK-;  
Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolated from  
the testes of 31 male adult zebrafish (4-5 month old).  
cDNAs were made using oligo-dT primers and inserted into  
lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo  
mass-excised to pBluescript SK- following the Washington  
University protocol  
(http://genome.wustl.edu/est/lambda_protocol.shtml).  
Please contact Zhiyuan Gong for further information on  
this library (National University of Singapore,  
Department of Biological Sciences, Lower Kent Ridge Road,  
Singapore 119260)."
```

BASE COUNT 179 a 106 c 154 g 135 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 13; Length 574;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCT 18
|||||
Db 430 CTGGGCCATCAGTCTCT 413

RESULT 36 591 bp mRNA linear EST 13-FEB-2002
B1670955 LOCUS
DEFINITION fp58f06.x1 Zebrafish adult retina cDNA Danio rerio cDNA clone
IMAGE:4786307 3' similar to SW:IAIP_CHICK Q90660 INHIBITOR OF
APOPTOSIS PROTEIN ;, mRNA sequence.
ACCESSION B1670955
VERSION B1670955.1 GI:15586339
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 591)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.
TITLE Washu Zebrafish EST Project 1998
JOURNAL Unpublished
COMMENT Other ESTs: fp58f06.y1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
Library constructed by: Chandra Tucker and Gregory Niemi DNA
Sequencing by: Washington University Genome Sequencing Center Clome
distribution: RessourcenzentrumPrimaDatenbank, Berlin, Germany
(web address: www.rzpd.de)
Seq primer: T7 from Gibco
High quality sequence stop: 389.
location/Qualifiers
1..591
/organism="Danio rerio"
/mol_type="mRNA"
/strain="wild-type"
/db_xref="taxon:7955"
/clone="IMAGE:4786307"
/sex="mixed"
/dev_stage="1-2 years"
/lab_host="B.Coli XL1-Blue MRF' (XL1-Blue MRF')"
/clone_lib="Zebrafish adult retina cDNA"
/note="Vector: Lambda ZAP II (pBluescript SK-); Site_1:

ECORI; Site_2: SalI; This zebrafish library was constructed by Dr. Susan E. Brockerhoff (email: sbrocker@u.washington.edu) RZPD library number: 760"

Query Match 86.3%; Score 16.4; DB 12; Length 591;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CTGGGCCATCAGTCTCT 18
Db 263 CTGGGCCATCAGTCTCT 280

RESULT 37
CA500347/c 596 bp mRNA linear EST 14-NOV-2002

LOCUS WHE4018_D05_G10ZT wheat meiotic anther cDNA library Triticum
DEFINITION aestivum cDNA clone WHE4018_D05_G10, mRNA sequence.

ACCESSION CA500347
VERSION CA500347.1 GI:24991307

KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)

ORGANISM

REFERENCE
AUTHORS Anderson, O.D., Chao, S., Crossman, C., Langridge, P., Lazo, G.R., Pham, J., Rausch, C.J., Sutton, T., Woo, J., and Wilson, C.

TITLE The structure and function of the expressed portion of the wheat
JOURNAL genomes - Meiotic anther cDNA library
COMMENT Unpublished

CONTACT: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov

Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: T7 primer.

FEATURES
Location/Qualifiers

1..596

/organism="Triticum aestivum"

/mol_type="mRNA"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="WHE4018_D05_G10"

/tissue_type="Anther"

/dev_stage="Meiotic stages pre-meiosis-metaphase I"

/lab_host="E. coli DH10B"

/note="Vector: pSPORT1, Site_1: SalI; Site_2: NotI; Plants

were grown in a glasshouse. Anther meiotic stage was

determined by removing anthers from individual primary

florets. One anther was sacrificed for microscopic staging

, and if determined to be between (and including) meiotic

stages pre-meiosis and metaphase I, the remaining two

anthers were collected and pooled for library

construction. The tissue, total RNA, and poly(A) RNA were

prepared, cDNA synthesised, and directionally ligated into

pSPORT1 by Tim Sutton in the P Langridge lab at the

Department of Plant Science, University of Adelaide, Waite

Campus, Australia. Average insert size 1.5Kb. Plasmid DNA

preparations and DNA sequencing were performed in the OD

Anderson lab (all other authors)."

BASE COUNT 200 a 119 c 164 g 113 t

Query Match 86.3%; Score 16.4; DB 14; Length 596;

Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CTGGGCCATCAGTCTCT 18
Db 552 CTGGGCCATCAGTCTCT 535

RESULT 38
AI496684/c 602 bp mRNA linear EST 07-JUN-2001

LOCUS fb48e09.y1 Zebrafish Washu MPMG EST Danio rerio cDNA clone
DEFINITION IMAGE:3715144 5' similar to SW:IAF_CHICK_Q90660 INHIBITOR OF

APOPTOSIS PROTEIN ;, mRNA sequence.

ACCESSION AI496684

VERSION AI496684.1 GI:4397687

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM

REFERENCE
AUTHORS Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.

1 (bases 1 to 602)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepec, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.

Washu Zebrafish EST Project 1998

TITLE Unpublished

JOURNAL

COMMENT

Contact: Stephen L. Johnson
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu

cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Washington University Genome

Sequencing Center Clone distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

info@genomesystems.com) and Research Genetics, Huntsville, Alabama

(web address: www.reegen.com) (email contact: info@reegen.com) and

RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:

www.rzp.d.de)

Possible reversed clone: similarity on wrong strand

Seq primer: T3 ET from Amersham

High quality sequence stop: 482

POLYA=No.

FEATURES
Location/Qualifiers

1..602

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:3715144"

/sex="mixed"

/tissue_type="26 somite embryos, adult livers, shield

stage embryos"

/lab_host="XLI-blue MRF"

/clone_lib="Zebrafish Washu MPMG EST"

/note="Vector: pSPORT1, Site_1: NotI; Site_2: SalI; 1st

strand cDNA was primed with a Not I - oligo(dT)15 primer

[5'GACTAGTCTTAGATCGGAGCGGCGCCCTTTTCTTTTCTTT3'];

double-stranded cDNA was ligated to Sal I adaptors (BRL),

digested with Not I and cloned into the Not I and Sal I

sites of the pSPORT1 vector (BRL). Library was constructed

by Matthew Clark (Lehrach lab; ICRF, London and Max Planck

Institut fuer Molekulare Genetik, Berlin). cDNAs for EST

analysis were selected following oligonucleotide

hybridization fingerprinting of arrayed clones from

zebrafish late somitogenesis (26 ss), adult liver or

embryonic shield stage (5.6 h) libraries. Fingerprint

data were used to computationally cluster cDNAs, and a

single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."

BASE COUNT 179 a 123 c 154 g 146 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 9; Length 602;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCT 18

Db 374 CTGGCCATCAGTCTCT 357

RESULT 39 627 bp mRNA linear EST 02-APR-2002
BQ074707
LOCUS f224f09.x1 Gong zebrafish testis Danio rerio cDNA 3' similar to
DEFINITION SW:1AP_CHICK Q90660 INHIBITOR OF APOPTOSIS PROTEIN ;, mRNA
sequence.

ACCESSION BQ074707 GI:19903744

VERSION BQ074707
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)

ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes ; Cyprinidae; Danio.
1 (bases 1 to 627)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Washu Zebrafish EST Project 1998

TITLE
JOURNAL
COMMENT

Unpublished

Other ESTs: f224f09.y1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu
The library was constructed by Dr. Z. Gong. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis. Please contact Zhiyuan Gong for further information on this library (National University of Singapore, Department of Biological Sciences, Lower Kent Ridge Road, Singapore 119260).

Seq primer: T7 from Gibco
High quality sequence stop: 473.

FEATURES
location/Qualifiers

source

1..627
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/sex="male"
/dev_stage="4-5 month"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Gong zebrafish testis"
/note="Organ: testis (pooled); Vector: pBluescript SK-; Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolated from the testes of 31 male adult zebrafish (4-5 month old). cDNAs were made using oligo-dT primers and inserted into lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo mass-excised to pBluescript SK- following the Washington University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Zhiyuan Gong for further information on this library (National University of Singapore,

Department of Biological Sciences, Lower Kent Ridge Road, Singapore 119260)."

BASE COUNT 149 a 156 c 119 g 203 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 13; Length 627;
Best Local Similarity 94.4%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCT 18

Db 265 CTGGCCATCAGTCTCT 282

RESULT 40 672 bp mRNA linear EST 30-AUG-2000
BE557791

LOCUS f110g10.y1 Zebrafish Research Genetics C32 fin Danio rerio cDNA 5' similar to SW:1AP2_HUMAN Q13490 INHIBITOR OF APOPTOSIS PROTEIN 2 ;, mRNA sequence.

ACCESSION BE557791 GI:9822281

VERSION BE557791

KEYWORDS EST.
SOURCE Danio rerio (zebrafish)

ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes ; Cyprinidae; Danio.
1 (bases 1 to 672)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Washu Zebrafish EST Project 1998

TITLE
JOURNAL
COMMENT

Unpublished

Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Ning Wu. cDNA Library Arrayed by: Research Genetics. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Research Genetics web address: http://www.researchgenetics.com/
Seq primer: T3 ET from Amersham
High quality sequence stop: 465.

FEATURES
location/Qualifiers

source

1..672
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/cissue_type="fin"
/lab_host="GeneHogs (HS996, a phage-resistant isolate of DH10B)"
/clone_lib="Zebrafish Research Genetics C32 fin"
/note="Vector: pT7T3D-Pac with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was prepared from zebrafish(C32) fin, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is non-normalized. Library was constructed by Ning Wu. NOTE: This clone is available royalty-free through LNL; contact the IMAGE Consortium (info.lnl.gov) for further information"

BASE COUNT 159 a 181 c 127 g 205 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 10; Length 672;
Best Local Similarity 94.4%; Pred. No. 3e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGCCCATCAGTCTCT 18
|||
Db 220 CTGGGCCCATCAGTCTCT 237

Search completed: January 13, 2004, 16:33:23
Job time : 1196.5 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2004, 17:32:17 ; Search time 126.5 Seconds
(without alignments)
521.578 Million cell updates/sec

Title: US-09-719-737-18
Perfect score: 19
Sequence: 1 ctgggccatcagtgctctg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2276164 seqs, 1736306516 residues

Total number of hits satisfying chosen parameters: 4552328

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	591	US-10-029-386-9548	Sequence 9548, Ap
2	19	100.0	1065	US-09-922-895-2	Sequence 2, Appli
3	19	100.0	1068	US-10-276-950-2	Sequence 2, Appli
4	19	100.0	1068	US-09-826-509-474	Sequence 474, App
5	19	100.0	1071	US-10-293-050-6	Sequence 6, Appli
6	19	100.0	1116	US-10-283-028-5	Sequence 5, Appli
7	19	100.0	1193	US-10-283-028-3	Sequence 3, Appli
8	19	100.0	1201	US-10-225-567A-63	Sequence 63, Appli
9	19	100.0	1689	US-09-931-381A-15	Sequence 15, Appli
10	19	100.0	1689	US-10-283-028-1	Sequence 1, Appli
11	19	100.0	1717	US-09-964-824A-100	Sequence 100, App
12	19	100.0	1915	US-10-106-623-3	Sequence 3, Appli
13	19	100.0	3426	US-10-001-835-29	Sequence 29, Appli
14	17.4	91.6	549	US-09-864-761-9611	Sequence 9611, Ap
15	17.4	91.6	563	US-10-029-386-152	Sequence 152, App

C	16	17.4	91.6	1516	10	US-09-745-605-2	Sequence 2, Appli
	17	16	84.2	824	13	US-10-027-632-136447	Sequence 136447,
	18	16	84.2	824	13	US-10-027-632-165611	Sequence 165611,
	19	16	84.2	824	14	US-10-027-632-136447	Sequence 136447,
	20	16	84.2	824	14	US-10-027-632-165611	Sequence 165611,
C	21	15.8	83.2	445	13	US-10-188-619-14	Sequence 14, Appli
C	22	15.8	83.2	145	11	US-09-747-377-447	Sequence 447, App
C	23	15.8	83.2	145	15	US-10-105-613-447	Sequence 447, App
	24	15.8	83.2	422	10	US-09-920-300A-583	Sequence 583, App
	25	15.8	83.2	422	13	US-10-099-926-583	Sequence 583, App
	26	15.8	83.2	422	14	US-10-033-528-583	Sequence 583, App
C	27	15.8	83.2	492	13	US-10-027-632-281562	Sequence 281562,
C	28	15.8	83.2	492	13	US-10-027-632-281563	Sequence 281562,
C	29	15.8	83.2	492	14	US-10-027-632-281562	Sequence 281562,
C	30	15.8	83.2	492	14	US-10-027-632-281563	Sequence 281563,
	31	15.8	83.2	652	13	US-10-027-632-81346	Sequence 81346, A
	32	15.8	83.2	652	13	US-10-027-632-81347	Sequence 81347, A
	33	15.8	83.2	652	13	US-10-027-632-109771	Sequence 109771,
	34	15.8	83.2	652	13	US-10-027-632-109772	Sequence 109772,
	35	15.8	83.2	652	13	US-10-027-632-301812	Sequence 301812,
	36	15.8	83.2	652	13	US-10-027-632-301813	Sequence 301813,
	37	15.8	83.2	652	14	US-10-027-632-81346	Sequence 81346, A
	38	15.8	83.2	652	14	US-10-027-632-81347	Sequence 81347, A
	39	15.8	83.2	652	14	US-10-027-632-109771	Sequence 109771,
	40	15.8	83.2	652	14	US-10-027-632-109772	Sequence 109772,
	41	15.8	83.2	652	14	US-10-027-632-301812	Sequence 301812,
	42	15.8	83.2	652	14	US-10-027-632-301813	Sequence 301813,
C	43	15.8	83.2	1025	13	US-10-027-632-262488	Sequence 262488,
C	44	15.8	83.2	1025	13	US-10-027-632-262489	Sequence 262489,
C	45	15.8	83.2	1025	14	US-10-027-632-262488	Sequence 262488,

ALIGNMENTS

RESULT 1
US-10-029-386-9548/C
; Sequence 9548, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9548
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR3.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
; OTHER INFORMATION: SWISSPROT HIT: P51677, EVALU 1.00e-102
; OTHER INFORMATION: NT HIT: g111449889, EVALU 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: BG182330.1, EVALU 0.00e+00
US-10-029-386-9548

Query Match 100.0%; Score 19; DB 13; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTGCTCTG 19
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Db 59 CTGGCCATCAGTCTCTG 41

RESULT 2

US-09-922-895-2/c

; Sequence 2, Application US/09922895
; Publication No. US20020192214A1

GENERAL INFORMATION:

APPLICANT: DAUGHERTY, BRUCE L.
DEMARTINO, JULIE A.
SICILIANO, SALVATORE J.
SPRINGER, MARTIN J.

TITLE OF INVENTION: EOSINOPHIL EOTAXIN RECEPTOR

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSES: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/922,895

FILING DATE: 06-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/847,296

FILING DATE: <Unknown>

APPLICATION NUMBER: 60/017,113

FILING DATE: 26-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Thies, J. Eric

REGISTRATION NUMBER: 35,382

REFERENCE/DOCKET NUMBER: 19634Y

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-594-3904

TELEFAX: 908-594-4720

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1065 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-922-895-2

Query Match 100.0%; Score 19; DB 10; Length 1065;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
|||||
Db 105 CTGGCCATCAGTCTCTG 87

RESULT 3

US-10-276-950-2/c

; Sequence 2, Application US/10276950
; Publication No. US20030157639A1

GENERAL INFORMATION:

APPLICANT: GLAXO GROUP LIMITED

TITLE OF INVENTION: PROTEIN AND ASSAY

FILE REFERENCE: PG3810

CURRENT APPLICATION NUMBER: US/10/276,950

PRIOR FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: GB 0013345.4

; PRIOR FILING DATE: 2000-06-01

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 1068

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1068)

US-10-276-950-2

Query Match

Best Local Similarity 100.0%; Score 19; DB 13; Length 1068;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
|||||
Db 105 CTGGCCATCAGTCTCTG 87

RESULT 4

US-09-826-509-474/c

; Sequence 4/74, Application US/09826509
; Publication No. US20030204073A1

GENERAL INFORMATION:

APPLICANT: Lehmann-Bruinsma, Karin

APPLICANT: Liaw, Chen W.

APPLICANT: Lin, I-Lin

TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

FILE REFERENCE: AREN-207

CURRENT APPLICATION NUMBER: US/09/826,509

CURRENT FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 60/195,747

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: 09/170,496

PRIOR FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 589

SOFTWARE: PatentIn Version 2.1

SEQ ID NO 474

LENGTH: 1068

TYPE: DNA

ORGANISM: Homo sapiens

US-09-826-509-474

Query Match

Best Local Similarity 100.0%; Score 19; DB 13; Length 1068;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
|||||
Db 105 CTGGCCATCAGTCTCTG 87

RESULT 5

US-10-293-050-6/c

; Sequence 6, Application US/10293050
; Publication No. US20030130494A1

GENERAL INFORMATION:

APPLICANT: Dairaghi, Daniel J.

APPLICANT: Hara, Takahiko

APPLICANT: Miyajima, Atsushi

APPLICANT: Schall, Thomas J.

APPLICANT: Wang, Wei

APPLICANT: Yoshimura, Akihiko

TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS

FILE REFERENCE: DX0506B US

CURRENT APPLICATION NUMBER: US/10/293,050

CURRENT FILING DATE: 2003-02-11

PRIOR APPLICATION NUMBER: US 08/567,882

PRIOR FILING DATE: 1995-12-08

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 1071
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1071)
OTHER INFORMATION:
US-10-293-050-6

Query Match 100.0%; Score 19; DB 16; Length 1071;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTGTCTG 19
|||
Db 105 CTGGCCATCAGTGTCTG 87

RESULT 6
US-10-283-028-5/c

Sequence 5, Application US/10283028
Publication No. US20030143684A1

GENERAL INFORMATION:

APPLICANT: Gerard, Craig J.

Gerard, No. US20030143684A1ma P.

Mackay, Charles R.

Ponath, Paul D.

Post, Theodore W.

Qin, Shixin

TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
ANTAGONISTS THEREOF

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/283,028

FILING DATE: 28-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/720,565

FILING DATE: 30-SEP-1996

APPLICATION NUMBER: PCT/US96/00608

FILING DATE: 19-JAN-1996

APPLICATION NUMBER: US 08/375,199

FILING DATE: 19-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: LKS94-05A2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1116 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-283-028-5

Query Match 100.0%; Score 19; DB 13; Length 1116;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTGTCTG 19
|||
Db 119 CTGGCCATCAGTGTCTG 101

RESULT 7

US-10-283-028-3/c

Sequence 3, Application US/10283028

Publication No. US20030143684A1

GENERAL INFORMATION:

APPLICANT: Gerard, Craig J.

Gerard, No. US20030143684A1ma P.

Mackay, Charles R.

Ponath, Paul D.

Post, Theodore W.

Qin, Shixin

TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
ANTAGONISTS THEREOF

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/283,028

FILING DATE: 28-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/720,565

FILING DATE: 30-SEP-1996

APPLICATION NUMBER: PCT/US96/00608

FILING DATE: 19-JAN-1996

APPLICATION NUMBER: US 08/375,199

FILING DATE: 19-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: LKS94-05A2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1193 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 92..1156

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-283-028-3

Query Match 100.0%; Score 19; DB 13; Length 1193;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTGTCTG 19
|||
Db 196 CTGGCCATCAGTGTCTG 178

RESULT 8
US-10-225-567A-63/c
; Sequence 63, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 1201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-63

Query Match 100.0%; Score 19; DB 15; Length 1201;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCATCAGTGTCTG 19
|||||
DB 136 CTGGGCATCAGTGTCTG 118

RESULT 9
US-09-931-381A-15/c
; Sequence 15, Application US/09931381A
; Patent No. US20020137107A1
; GENERAL INFORMATION:
; APPLICANT: Butcher, Eugene C.
; APPLICANT: Kunkel, Eric J.
; APPLICANT: Pan, Junliang
; APPLICANT: Soler-Ferran, Dulce
; TITLE OF INVENTION: Method for Identifying Agents Which
; TITLE OF INVENTION: Modulate Chemokine "MCC"-Induced Functions of CCR3 and/or
; TITLE OF INVENTION: CCR10
; FILE REFERENCE: 1855.2010-003
; CURRENT APPLICATION NUMBER: US/09/931,381A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: U.S. 09/638,914
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (181)...(1248)
; NAME/KEY: misc feature
; LOCATION: (1291)...(1291)
; OTHER INFORMATION: n = A, T, C or G
US-09-931-381A-15

Query Match 100.0%; Score 19; DB 10; Length 1689;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCATCAGTGTCTG 19
|||||
DB 285 CTGGGCATCAGTGTCTG 267

RESULT 10
US-10-283-028-1/c
; Sequence 1, Application US/10283028
; Publication No. US20030143684A1
; GENERAL INFORMATION:
; APPLICANT: Gerard, Craig J.
; Gerard, No. US20030143684A1ma P.
; Mackay, Charles R.
; Ponath, Paul D.
; Post, Theodore W.
; Qin, Shixin
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
; ANTAGONISTS THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,028
; FILING DATE: 28-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,565
; FILING DATE: 30-SEP-1996
; APPLICATION NUMBER: PCT/US96/00608
; FILING DATE: 19-JAN-1996
; APPLICATION NUMBER: US 08/375,199
; FILING DATE: 19-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS94-05A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-283-028-1

Query Match 100.0%; Score 19; DB 13; Length 1689;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCATCAGTGTCTG 19
|||||
DB 285 CTGGGCATCAGTGTCTG 267

RESULT 11
US-09-964-824A-100/c
; Sequence 100, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatur
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 6892290-73


```
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 100
; LENGTH: 1717
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-100

Query Match      100.0%; Score 19; DB 10; Length 1717;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGGGCCATCAGTGTCTG 19
Db      309 CTGGGCCATCAGTGTCTG 291

RESULT 12
US-10-106-623-3/c
; Sequence 3, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
;           Schweickart, Vicki L.
;           Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1915 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 362..1426
; FEATURE:
; NAME/KEY: misc_feature
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```
; OTHER INFORMATION: /= "88-2B polynucleotide and amino acid
; sequences"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-106-623-3

Query Match      100.0%; Score 19; DB 14; Length 1915;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGGGCCATCAGTGTCTG 19
Db      466 CTGGGCCATCAGTGTCTG 448

RESULT 13
US-10-001-835-29/c
; Sequence 29, Application US/10001835
; Publication No. US20020160387A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Heve
; APPLICANT: Cafferey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Prot
; FILE REFERENCE: DEX-0277
; CURRENT APPLICATION NUMBER: US/10/001,835
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,997
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 3426
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-835-29

Query Match      100.0%; Score 19; DB 14; Length 3426;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTGGGCCATCAGTGTCTG 19
Db      234 CTGGGCCATCAGTGTCTG 216

RESULT 14
US-09-864-761-9611/c
; Sequence 9611, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
```

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9611
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO Z83844.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; US-09-864-761-9611

Query Match          91.6%; Score 17.4; DB 9; Length 549;
Best Local Similarity 94.7%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGGCCATCAGTCTCTG 19
        |||||
Db      101 CTGGCCATGAGTCTCTG 83

RESULT 15
US-10-029-386-152/c
; Sequence 152, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 152
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR22_83.0
```

```
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: NT HIT: 915147251, EVALUE 4.00e-51
; OTHER INFORMATION: EST_HUMAN HIT: BG821494.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P56591, EVALUE 7.00e+00
; US-10-029-386-152

Query Match          91.6%; Score 17.4; DB 13; Length 563;
Best Local Similarity 94.7%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGGCCATCAGTCTCTG 19
        |||||
Db      74 CTGGCCATGAGTCTCTG 56

RESULT 16
US-09-745-605-2/c
; Sequence 2, Application US/09745605
; Patent No. US20020123617A1
; GENERAL INFORMATION:
; APPLICANT: Starling, Gary C.
; APPLICANT: Finger, Joshua N.
; TITLE OF INVENTION: NOVEL IMMUNOGLOBIN SUPERFAMILY MEMBERS APEX-1, APEX-2,
; FILE REFERENCE: DB13NP
; CURRENT APPLICATION NUMBER: US/09/745,605
; FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/172,025
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1516
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-745-605-2

Query Match          91.6%; Score 17.4; DB 10; Length 1516;
Best Local Similarity 94.7%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CTGGCCATCAGTCTCTG 19
        |||||
Db      1023 CTGGCCATCTGTCTCTG 1005

RESULT 17
US-10-027-632-136447
; Sequence 136447, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
```

```
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136447
; LENGTH: 824
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-136447
```

```
Query Match      84.2%; Score 16; DB 13; Length 824;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 GGCATCAGTGTCTG 19
         |||||
Db      342 GGCATCAGTGTCTG 357
```

```
RESULT 18
US-10-027-632-165611
; Sequence 165611, Application US/10027632
; Publication No. US20030204075a9
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
```

```
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
```

```
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

```
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
```

```
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
```

```
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
```

```
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
```

```
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
```

```
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
```

```
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165611
```

```
; LENGTH: 824
; TYPE: DNA
```

```
; ORGANISM: Human
US-10-027-632-165611
```

```
Query Match      84.2%; Score 16; DB 13; Length 824;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 GGCATCAGTGTCTG 19
         |||||
Db      342 GGCATCAGTGTCTG 357
```

```
RESULT 19
US-10-027-632-136447
; Sequence 136447, Application US/10027632
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
```

```
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
```

```
; CURRENT APPLICATION NUMBER: US/10/027,632
```

```
; CURRENT FILING DATE: 2002-04-30
```

```
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

```
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
```

```
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
```

```
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
```

```
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
```

```
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
```

```
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
```

```
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136447
```

```
; LENGTH: 824
; TYPE: DNA
```

```
; ORGANISM: Human
US-10-027-632-136447
```

```
Query Match      84.2%; Score 16; DB 14; Length 824;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 GGCATCAGTGTCTG 19
         |||||
Db      342 GGCATCAGTGTCTG 357
```

```
RESULT 20
US-10-027-632-165611
; Sequence 165611, Application US/10027632
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
```

```
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
```

```
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

```
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
```

```
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
```

```
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
```

```
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
```

```
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
```

```
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
```

```
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165611
```

```
; LENGTH: 824
; TYPE: DNA
```

```
; ORGANISM: Human
US-10-027-632-165611
```

```
Query Match      84.2%; Score 16; DB 14; Length 824;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 GGCATCAGTGTCTG 19
         |||||
Db      342 GGCATCAGTGTCTG 357
```

```

RESULT 21
US-10-188-619-14/c
; Sequence 14, Application US/10188619
; Publication No. US20030162944A1
; GENERAL INFORMATION:
; APPLICANT: Christophe P.G. Gerald, et al.
; TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/188,619
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/407,367
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44742-AA-PCT-US/JPW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-10-188-619-14

Query Match      83.2%; Score 15.8; DB 13; Length 45;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CTGGGCATCAGTGCCTG 19
      ||||| ||||| ||||| |||
Db      43 CTGGGCATCAGTGCCTG 25

RESULT 22
US-09-747-377-447/c
; Sequence 447, Application US/09747377
; Publication No. US20030022255A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR BREAST CANCER
; FILE REFERENCE: A-69959/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/747,377
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 493
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 447
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Mus sp.
US-09-747-377-447

```

Query Match	83.2%;	Score 15.8;	DB 11;	Length 145;
Best Local Similarity	89.5%;	Pred. No. 1.5e+02;		
Matches 17;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	CTGGGCCATCAGTGCTCTG	19	
Db	49	CTTGGCCATCTGTGCTCTG	31	

```

RESULT 23
US-10-105-613-447/C
; Sequence 447, Application US/10105613
; Publication No. US2003009963A1
; GENERAL INFORMATION:
; APPLICANT: MORRIS, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR BREAST CANCER
; FILE REFERENCE: A-69959/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/105,613
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US/09/747,377
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 493
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 447
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Mus sp.
US-10-105-613-447

```

Query Match	83.2%;	Score 15.8;	DB 15;	length 145;
Best Local Similarity	89.5%;	Pred. No. 1.5e+02;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	CTGGCCATCAGTGTCTTG	19	
DB	49	CTGGCCATCTGTGCTCTG	31	

```

RESULT 24
US-09-920-300A-583
; Sequence 583, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 583
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-583

```

Query Match	83.2%	Score 15.8;	DB 10;	Length 422;
Best Local Similarity	89.5%;	Pred. No. 1.5e+02;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	CTGGCCATGACTGCTCTG	19	
DB	237	CTGGCCATGACTGCTCTG	255	

RESULT 25
US-10-099-926-583
; Sequence 583, Application US/10099926
; Publication No. US20030166064A1

```
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C2
; CURRENT APPLICATION NUMBER: US/10/099,926
; CURRENT FILING DATE: 2002-03-17
; NUMBER OF SEQ ID NOS: 1982
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 583
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-099-926-583

Query Match      83.2%; Score 15.8; DB 13; Length 422;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CTGGGCATCAGTCTCTG 19
         ||||| ||||| ||||| |||||
Db      237 CTGGGCATGACTGCTCTG 255

RESULT 26
US-10-033-528-583
; Sequence 583, Application US/10033528
; Publication No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 583
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-583
```

```
Query Match      83.2%; Score 15.8; DB 14; Length 422;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CTGGGCATCAGTCTCTG 19
         ||||| ||||| ||||| |||||
Db      237 CTGGGCATGACTGCTCTG 255

RESULT 27
US-10-027-632-281562/c
; Sequence 281562, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
```

```
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281562
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-281562
```

```
Query Match      83.2%; Score 15.8; DB 13; Length 492;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CTGGGCATCAGTCTCTG 19
         ||||| ||||| ||||| |||||
Db      382 CTGGGCATGACTGCTCTG 364

RESULT 28
US-10-027-632-281563/c
; Sequence 281563, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281563
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-281563
```

```
Query Match      83.2%; Score 15.8; DB 13; Length 492;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CTGGGCATCAGTCTCTG 19
         ||||| ||||| ||||| |||||
Db      382 CTGGGCATGACTGCTCTG 364

RESULT 29
US-10-027-632-281562/c
; Sequence 281562, Application US/10027632
```

```
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 281562
LENGTH: 492
TYPE: DNA
ORGANISM: Human
US-10-027-632-281562
```

```
Query Match      83.2%; Score 15.8; DB 14; Length 492;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      1 CTGGCCATCAGTCTCTG 19
      |||||
Db      382 CTGGCCATCAGTCTCTG 364
```

```
RESULT 30
US-10-027-632-281563/c
Sequence 281563, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 281563
LENGTH: 492
TYPE: DNA
ORGANISM: Human
US-10-027-632-281563
```

```
Query Match      83.2%; Score 15.8; DB 14; Length 492;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      1 CTGGCCATCAGTCTCTG 19
      |||||
Db      382 CTGGCCATCAGTCTCTG 364
```

```
RESULT 31
US-10-027-632-81346
Sequence 81346, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 81346
LENGTH: 652
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(652)
OTHER INFORMATION: n = A,T,C or G
US-10-027-632-81346
```

```
Query Match      83.2%; Score 15.8; DB 13; Length 652;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      1 CTGGCCATCAGTCTCTG 19
      |||||
Db      339 CAGGCCATCAGGCTCTG 357
```

```
RESULT 32
US-10-027-632-81347
Sequence 81347, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
```

```
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81347
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(652)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-81347
```

```
Query Match      83.2%; Score 15.8; DB 13; Length 652;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CTGGGCCATCAGTCTCTG 19
      |||||
Db      339 CAGGGCCATCAGGCTCTG 357
```

```
RESULT 33
US-10-027-632-109771
; Sequence 109771, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109771
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(652)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-109771
```

```
Query Match      83.2%; Score 15.8; DB 13; Length 652;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CTGGGCCATCAGTCTCTG 19
      |||||
Db      339 CAGGGCCATCAGGCTCTG 357
```

```
RESULT 34
US-10-027-632-109772
```

```
; Sequence 109772, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109772
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(652)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-109772
```

```
Query Match      83.2%; Score 15.8; DB 13; Length 652;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CTGGGCCATCAGTCTCTG 19
      |||||
Db      339 CAGGGCCATCAGGCTCTG 357
```

```
RESULT 35
US-10-027-632-301812
; Sequence 301812, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 301812
; LENGTH: 652
```



```
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(652)
OTHER INFORMATION: n = A,T,C or G
US-10-027-632-301812
```

```
Query Match      83.2%; Score 15.8; DB 13; Length 652;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CTGGGCATCAGTCTCTG 19
      |||||
Db      339 CAGGGCCATCAGGCTCTG 357
```

RESULT 36

```
US-10-027-632-301813
Sequence 301813, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
```

```
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
```

```
FILE REFERENCE: 108827.129
```

```
CURRENT APPLICATION NUMBER: US/10/027,632
```

```
PRIOR FILING DATE: 2002-04-30
```

```
PRIOR APPLICATION NUMBER: US 60/218,006
```

```
PRIOR FILING DATE: 2000-07-12
```

```
PRIOR APPLICATION NUMBER: US 60/198,676
```

```
PRIOR FILING DATE: 2000-04-20
```

```
PRIOR APPLICATION NUMBER: US 60/193,483
```

```
PRIOR FILING DATE: 2000-03-29
```

```
PRIOR APPLICATION NUMBER: US 60/185,218
```

```
PRIOR FILING DATE: 2000-02-24
```

```
PRIOR APPLICATION NUMBER: US 60/167,363
```

```
PRIOR FILING DATE: 1999-11-23
```

```
PRIOR APPLICATION NUMBER: US 60/156,358
```

```
PRIOR FILING DATE: 1999-09-28
```

```
PRIOR APPLICATION NUMBER: US 60/146,002
```

```
PRIOR FILING DATE: 1999-08-09
```

```
NUMBER OF SEQ ID NOS: 325720
```

```
SOFTWARE: FastSeq for windows Version 4.0
```

```
SEQ ID NO 301813
```

```
LENGTH: 652
```

```
TYPE: DNA
```

```
ORGANISM: Human
```

```
FEATURE:
```

```
NAME/KEY: misc_feature
```

```
LOCATION: (1)...(652)
```

```
OTHER INFORMATION: n = A,T,C or G
```

```
US-10-027-632-301813
```

```
Query Match      83.2%; Score 15.8; DB 13; Length 652;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
```

```
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 CTGGGCATCAGTCTCTG 19
      |||||
Db      339 CAGGGCCATCAGGCTCTG 357
```

RESULT 37

```
US-10-027-632-81346
```

```
Sequence 81346, Application US/10027632
```

```
GENERAL INFORMATION:
```

```
APPLICANT: Wang, David G.
```

```
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```

```
Polymorphisms in the Human Genome
```

```
FILE REFERENCE: 108827.129
```

```
CURRENT APPLICATION NUMBER: US/10/027,632
```

```
PRIOR FILING DATE: 2002-04-30
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for windows Version 4.0
SEQ ID NO 81346
LENGTH: 652
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(652)
OTHER INFORMATION: n = A,T,C or G
US-10-027-632-81346
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Query Match      83.2%; Score 15.8; DB 14; Length 652;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 CTGGGCATCAGTCTCTG 19
      |||||
Db      339 CAGGGCCATCAGGCTCTG 357
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RESULT 38

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US-10-027-632-81347
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Sequence 81347, Application US/10027632
```

```
GENERAL INFORMATION:
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```
APPLICANT: Wang, David G.
```

```
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```

```
Polymorphisms in the Human Genome
```

```
FILE REFERENCE: 108827.129
```

```
CURRENT APPLICATION NUMBER: US/10/027,632
```

```
PRIOR FILING DATE: 2002-04-30
```

```
PRIOR APPLICATION NUMBER: US 60/218,006
```

```
PRIOR FILING DATE: 2000-07-12
```

```
PRIOR APPLICATION NUMBER: US 60/198,676
```

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PRIOR FILING DATE: 2000-04-20
```

```
PRIOR APPLICATION NUMBER: US 60/193,483
```

```
PRIOR FILING DATE: 2000-03-29
```

```
PRIOR APPLICATION NUMBER: US 60/185,218
```

```
PRIOR FILING DATE: 2000-02-24
```

```
PRIOR APPLICATION NUMBER: US 60/167,363
```

```
PRIOR FILING DATE: 1999-11-23
```

```
PRIOR APPLICATION NUMBER: US 60/156,358
```

```
PRIOR FILING DATE: 1999-09-28
```

```
PRIOR APPLICATION NUMBER: US 60/146,002
```

```
PRIOR FILING DATE: 1999-08-09
```

```
NUMBER OF SEQ ID NOS: 325720
```

```
SOFTWARE: FastSeq for windows Version 4.0
```

```
SEQ ID NO 81347
```

```
LENGTH: 652
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TYPE: DNA
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ORGANISM: Human
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```
FEATURE:
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```
NAME/KEY: misc_feature
```

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LOCATION: (1)...(652)
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OTHER INFORMATION: n = A,T,C or G
```

```
US-10-027-632-81347
```

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Query Match      83.2%; Score 15.8; DB 14; Length 652;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
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	Matches	17; Conservative	0; Mismatches	2; Indels	0; Gaps
Qy	1	CTGGGCCATCAGTGTCTG	19		
Db	339	CAGGGCCATCAGGGCTCTG	357		

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RESULT 39
US-10-027-632-109771
; Sequence 109771, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109771
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(652)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-109771

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Query Match	83.2%;	Score 15.8;	DB 14;	Length 652;
Best Local Similarity	89.5%;	Pred. No. 1.5e+02;		
Matches 17;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

```

QY      1 CTGGCCATCAGTCTCTG 19
          |||||
Db      339 CAGGCCATCAGGCTCTG 357

```

```

RESULT 40
US-10-027-632-109772
; Sequence 109772, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

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; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109772
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(652)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-109772

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Query Match	83.2%;	Score 15.8;	DB 14;	Length 652;
Best Local Similarity	89.5%;	Pred. No. 1.5e+02;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
DB 339 CAGGCCATCAGGCTCTG 357

Search completed: January 13, 2004, 21:03:12
Job time : 127.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2004, 15:53:18 ; Search time 36.5 Seconds
(without alignments)
229.761 Million cell updates/sec

Title: US-09-719-737-18
Perfect score: 19
Sequence: 1 ctggcgcatcagtgctctg 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCtUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	19	100.0	1065	3	US-08-847-296B-2	Sequence 2, Appl1
C 2	19	100.0	1071	4	US-08-567-882-6	Sequence 6, Appl1
C 3	19	100.0	1116	4	US-08-720-565-5	Sequence 5, Appl1
C 4	19	100.0	1193	4	US-08-720-565-3	Sequence 3, Appl1
C 5	19	100.0	1201	4	US-09-016-434-1085	Sequence 1085, Ap
C 6	19	100.0	1689	4	US-08-720-565-1	Sequence 1, Appl1
C 7	19	100.0	1915	3	US-08-575-967A-3	Sequence 3, Appl1
C 8	15.8	83.2	45	2	US-08-687-355A-14	Sequence 14, Appl
C 9	15.8	83.2	45	4	US-09-016-434-1062	Sequence 1062, Ap
C 10	15.8	83.2	1280	1	US-08-192-288-1	Sequence 1, Appl1
C 11	15.8	83.2	1280	2	US-08-687-355A-1	Sequence 1, Appl1
C 12	15.8	83.2	1280	4	US-09-407-367-1	Sequence 1, Appl1
C 13	15.8	83.2	1786	3	US-09-015-296-2	Sequence 2, Appl1
C 14	15.8	83.2	1786	4	US-09-593-722-2	Sequence 2, Appl1
C 15	15.8	83.2	2144	4	US-08-876-798A-1	Sequence 1, Appl1
C 16	15.8	83.2	2144	4	US-08-876-798A-3	Sequence 3, Appl1
C 17	15.8	83.2	32155	4	US-08-311-731A-1	Sequence 1, Appl1
C 18	15.4	81.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
C 19	15.4	81.1	441529	3	US-09-103-840A-1	Sequence 1, Appl1
C 20	15.4	81.1	441529	3	US-09-168-629-14	Sequence 14, Appl
C 21	15	78.9	2931	3	US-09-215-131-1	Sequence 1, Appl1
C 22	15	78.9	3966	3	US-09-222-734-1	Sequence 1, Appl1
C 23	15	78.9	3966	2	US-08-687-355A-13	Sequence 13, Appl
C 24	14.8	77.9	45	4	US-09-407-367-13	Sequence 13, Appl
C 25	14.8	77.9	45	4	US-09-465-901-15	Sequence 15, Appl
C 26	14.8	77.9	669	4	US-09-465-901-15	Sequence 15, Appl
C 27	14.8	77.9	669	4	US-09-465-901-35	Sequence 35, Appl

C 28	14.8	77.9	1500	4	US-09-685-462-1	Sequence 1, Appl1
C 29	14.8	77.9	1744	4	US-09-685-462-9	Sequence 9, Appl1
C 30	14.8	77.9	2239	4	US-09-581-831-1	Sequence 1, Appl1
C 31	14.8	77.9	2529	4	US-09-620-312D-688	Sequence 688, App
C 32	14.8	77.9	36412	4	US-08-311-731A-132	Sequence 132, App
C 33	14.4	75.8	20	1	US-08-742-023-15	Sequence 15, Appl
C 34	14.4	75.8	20	3	US-08-968-505-15	Sequence 15, Appl
C 35	14.4	75.8	264	4	US-09-016-434-481	Sequence 481, App
C 36	14.4	75.8	321	4	US-09-404-879A-327	Sequence 327, App
C 37	14.4	75.8	1071	4	US-09-620-312D-769	Sequence 769, App
C 38	14.2	74.7	20	4	US-09-198-452A-6823	Sequence 6823, Ap
C 39	14.2	74.7	132	3	US-09-461-697-114	Sequence 114, App
C 40	14.2	74.7	141	3	US-09-461-697-112	Sequence 112, App
C 41	14.2	74.7	216	3	US-09-461-697-104	Sequence 104, App
C 42	14.2	74.7	336	3	US-09-461-697-100	Sequence 100, App
C 43	14.2	74.7	510	3	US-09-461-697-96	Sequence 96, Appl
C 44	14.2	74.7	600	3	US-09-461-697-92	Sequence 92, Appl
C 45	14.2	74.7	607	3	US-08-889-502-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-08-847-296B-2/c
Sequence 2, Application US/08847296B
Patent No. 6271347
GENERAL INFORMATION:
APPLICANT: DAUGHERTY, BRUCE L.
APPLICANT: DEMARTINO, JULIE A.
APPLICANT: SICILIANO, SALVATORE J.
APPLICANT: SPRINGER, MARTIN J.
TITLE OF INVENTION: EOSINOPHIL EOTAXIN RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847, 296B
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016, 158
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 60/017, 113
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Thies, J. Eric
REGISTRATION NUMBER: 35,382
REFERENCE/DOCKET NUMBER: 19634Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3904
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-847-296B-2
Query Match 100.0%; Score 19; DB 3; Length 1065;

Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGCCATCAGTCTCTG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 105 CTGGCCATCAGTCTCTG 87

RESULT 2

US-08-567-882-6/c
; Sequence 6, Application US/08567882
; Patent No. 6512103
; GENERAL INFORMATION:
; APPLICANT: Dairaghi, Daniel J.
; APPLICANT: Hara, Takahiko
; APPLICANT: Miyajima, Atsushi
; APPLICANT: Schall, Thomas J.
; APPLICANT: Wang, Wei
; APPLICANT: Yoshimura, Akihiko
; TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,882
; FILING DATE: 08-DEC-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0506
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1071 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1071
US-08-567-882-6

Query Match 100.0%; Score 19; DB 4; Length 1071;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGCCATCAGTCTCTG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 105 CTGGCCATCAGTCTCTG 87

RESULT 3

US-08-720-565-5/c
; Sequence 5, Application US/08720565
; Patent No. 6537764
; GENERAL INFORMATION:
; APPLICANT: Gerard, Craig J.
; APPLICANT: Gerard, No. 6537764ma P.
; APPLICANT: Mackay, Charles R.

; APPLICANT: Ponath, Paul D.
; APPLICANT: Post, Theodore W.
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,565
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00608
; FILING DATE: 19-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375,199
; FILING DATE: 19-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS94-05A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1116 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-720-565-5

Query Match 100.0%; Score 19; DB 4; Length 1116;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGCCATCAGTCTCTG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 119 CTGGCCATCAGTCTCTG 101

RESULT 4

US-08-720-565-3/c
; Sequence 3, Application US/08720565
; Patent No. 6537764
; GENERAL INFORMATION:
; APPLICANT: Gerard, Craig J.
; APPLICANT: Gerard, No. 6537764ma P.
; APPLICANT: Mackay, Charles R.
; APPLICANT: Ponath, Paul D.
; APPLICANT: Post, Theodore W.
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 92..1156
US-08-720-565-3

Query Match 100.0%; Score 19; DB 4; Length 1193;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGGCCATCAGTCTCTG 19
Db 196 CTGGGCCATCAGTCTCTG 178

RESULT 5
US-09-016-434-1085/c
Sequence 1085, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1085:
SEQUENCE CHARACTERISTICS:
LENGTH: 1201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 91199579
US-09-016-434-1085

Query Match 100.0%; Score 19; DB 4; Length 1201;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGGGCCATCAGTCTCTG 19
Db 136 CTGGGCCATCAGTCTCTG 118

RESULT 6
US-08-720-565-1/c
Sequence 1, Application US/08720565
Patent No. 6537764
GENERAL INFORMATION:
APPLICANT: Gerard, Craig J.
APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Mackay, Charles R.
APPLICANT: Ponath, Paul D.
APPLICANT: Post, Theodore W.
APPLICANT: Qin, Shixin
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
TITLE OF INVENTION: ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-720-565-1

Query Match 100.0%; Score 19; DB 4; Length 1689;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
DB 285 CTGGGCCATCAGTCTCTG 267

RESULT 7
US-08-575-967A-3/c
Sequence 3, Application US/08575967A

PATENT No. 6265184
GENERAL INFORMATION:
APPLICANT: Gray et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6265184and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1915 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 362..1426
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: /= "88-2B polynucleotide and amino acid
US-08-575-967A-3

Query Match 100.0%; Score 19; DB 3; Length 1915;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
DB 466 CTGGGCCATCAGTCTCTG 448

RESULT 8
US-08-687-355A-14/c
Sequence 14, Application US/08687355A

PATENT No. 5989834
GENERAL INFORMATION:
APPLICANT: Synaptic Pharmaceutical Corporation
TITLE OF INVENTION: NUCLEIC ACID ENCODING NEUROPEPTIDE
TITLE OF INVENTION: Y/PEPTIDE YX (Y2) RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,355A
FILING DATE: No. 5989834ember 26, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44742-A-PCT/JPW/MAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-687-355A-14

Query Match 83.2%; Score 15.8; DB 2; Length 45;
Best Local Similarity 89.5%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
DB 43 CTGGGCCATCAGTCTCTG 25

RESULT 9
US-09-407-367-14/c
Sequence 14, Application US/09407367
PATENT No. 6420532
GENERAL INFORMATION:
APPLICANT: Christophe P.G. Gerald, et al.
TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2 SPECIFIC COMPO
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,367
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44742-AA-PCT-US/JPW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYBOTHEICAL: NO
ANTI-SENSE: NO
US-09-407-367-14

Query Match 83.2%; Score 15.8; DB 4; Length 45;
Best Local Similarity 89.5%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGGCATCAGTCTCTG 19
DB 43 CTGGGCATCAGTCCCTG 25

RESULT 10
US-09-016-434-1062
Sequence 1062, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1062:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1063633

US-09-016-434-1062

Query Match 83.2%; Score 15.8; DB 4; Length 1200;
Best Local Similarity 89.5%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGGCATCAGTCTCTG 19
DB 536 CTGGGCATCAGTCCCTG 554

RESULT 11
US-08-192-288-1
Sequence 1, Application US/08192288
Patent No. 5545549
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe
APPLICANT: Walker, Mary
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
TITLE OF INVENTION: Y/PEPTIDE YY (Y2) RECEPTOR AND USES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/192,288
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44742/JPW/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1280 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1185
US-08-192-288-1

Query Match 83.2%; Score 15.8; DB 1; Length 1280;
Best Local Similarity 89.5%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGGCATCAGTCTCTG 19
DB 558 CTGGGCATCAGTCCCTG 576

RESULT 12
US-08-687-355A-1
Sequence 1, Application US/08687355A
Patent No. 5989834

GENERAL INFORMATION:
APPLICANT: Syaptic Pharmaceutical Corporation
TITLE OF INVENTION: NUCLEIC ACID ENCODING NEUROPEPTIDE
TITLE OF INVENTION: Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,355A
FILING DATE: No. 5989834ember 26, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44742-A-PCT/JPW/MAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1280 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1185
US-08-687-355A-1

Query Match 83.2%; Score 15.8; DB 2; Length 1280;
Best Local Similarity 89.5%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGGCGCATCAGTCTCTG 19
Db 558 CTGGGCGCATCAGTCTCTG 576

RESULT 13
US-09-407-367-1
Sequence 1, Application US/09407367
Patent No. 6420532
GENERAL INFORMATION:
APPLICANT: Christophe P.G. Gerald, et al.
TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2 SPECIFIC COMPO
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,367
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44742-AA-PCT-US/JPW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1280 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1185
US-09-407-367-1

Query Match 83.2%; Score 15.8; DB 4; Length 1280;
Best Local Similarity 89.5%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGGCGCATCAGTCTCTG 19
Db 558 CTGGGCGCATCAGTCTCTG 576

RESULT 14
US-09-015-296-2/C
Sequence 2, Application US/09015296
Patent No. 6103471
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN BETA-ALANINE-PYRUVATE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,296
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0467 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:

OY 2 TGGGCCATCAGTCTCT 18
|||||
DB 3299247 TGGGCCATCGTCTCT 3299231

RESULT 21

US-09-168-629-14/c
; Sequence 14, Application US/09168629
; Patent No. 6242253
; GENERAL INFORMATION:
; APPLICANT: Karin, Michael
; APPLICANT: Didonato, Joseph A.
; APPLICANT: Rochwarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: Zandi, Ebrahim
; TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same
; FILE REFERENCE: P-UD 3295
; CURRENT APPLICATION NUMBER: US/09/168,629
; EARLIER FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,470
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 2931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(2306)
US-09-168-629-14

Query Match 78.9%; Score 15; DB 3; Length 2931;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGCCATCAGTGC 15
|||||
DB 2468 CTGGGCCATCAGTGC 2454

RESULT 22

US-09-215-131-1/c
; Sequence 1, Application US/09215131
; Patent No. 6030834
; GENERAL INFORMATION:
; APPLICANT: Chu, Keting
; APPLICANT: Pot, David
; TITLE OF INVENTION: IKK Beta Regulates Transcription Factors
; FILE REFERENCE: 1449.002
; CURRENT APPLICATION NUMBER: US/09/215,131
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3966
; TYPE: DNA
; ORGANISM: human
US-09-215-131-1

Query Match 78.9%; Score 15; DB 3; Length 3966;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGCCATCAGTGC 15
|||||
DB 2433 CTGGGCCATCAGTGC 2419

RESULT 23

US-09-222-734-1/c
; Sequence 1, Application US/09222734A

; Patent No. 6077701
; GENERAL INFORMATION:
; APPLICANT: Chu, Keting
; APPLICANT: Pot, David
; TITLE OF INVENTION: IKK-beta Regulates Transcription Factors
; FILE REFERENCE: 12441.78080
; CURRENT APPLICATION NUMBER: US/09/222,734A
; CURRENT FILING DATE: 1998-12-29
; EARLIER APPLICATION NUMBER: 09/215,131
; EARLIER FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 60/068,954
; EARLIER FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3966
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-222-734-1

Query Match 78.9%; Score 15; DB 3; Length 3966;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGCCATCAGTGC 15
|||||
DB 2433 CTGGGCCATCAGTGC 2419

RESULT 24

US-08-687-355A-13
; Sequence 13, Application US/08687355A
; Patent No. 5989834
; GENERAL INFORMATION:
; APPLICANT: Synaptic Pharmaceutical Corporation
; TITLE OF INVENTION: NUCLEIC ACID ENCODING NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,355A
; FILING DATE: No. 5989834ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44742-A-PCT/JPW/MAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-687-355A-13

Query Match 77.9%; Score 14.8; DB 2; Length 45;

PRIOR FILING DATE: 1997-12-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1500
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (20) ... (1258)
US-09-685-462-1

Query Match 77.9%; Score 14.8; DB 4; Length 1500;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGGCCATCAGTGTCTG 19
DB 1294 TGGGCTTCAAGTCGCTG 1277

RESULT 29
US-09-685-462-9/c
Sequence 9, Application US/09685462
Patent No. 6524833
GENERAL INFORMATION:
APPLICANT: Zon, Leonard I.
APPLICANT: Agarwal, Sadhana
APPLICANT: Best, Jennifer
APPLICANT: Vail, Brenda
TITLE OF INVENTION: Two Sterile-20 Kinase-like Proteins and
TITLE OF INVENTION: Methods of Use Thereof
FILE REFERENCE: 1242.1016-004
CURRENT APPLICATION NUMBER: US/09/685,462
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/591,083
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: PCT/US98/26116
PRIOR FILING DATE: 1998-12-09
PRIOR APPLICATION NUMBER: US 60/069,078
PRIOR FILING DATE: 1997-12-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 1744
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (302) ... (1597)
US-09-685-462-9

Query Match 77.9%; Score 14.8; DB 4; Length 1744;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGGCCATCAGTGTCTG 19
DB 1604 TGGGCTTCAAGTCGCTG 1587

RESULT 30
US-09-581-831-1
Sequence 1, Application US/09581831
Patent No. 6448020
GENERAL INFORMATION:
APPLICANT: TOFGARD, RUNE
APPLICANT: ZAPHIROPOULOS, PETER G.
APPLICANT: KOGERMAN, PRIT
APPLICANT: GRIMM, THOMAS
TITLE OF INVENTION: MOLECULES ASSOCIATED WITH THE HUMAN SUPPRESSOR OF FUSED
TITLE OF INVENTION: GENE
FILE REFERENCE: 50695-60568

CURRENT APPLICATION NUMBER: US/09/581,831
CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: PCT/SE98/02383
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 9704788-0
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 9802293-2
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2239
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (167) .. (1618)
US-09-581-831-1

Query Match 77.9%; Score 14.8; DB 4; Length 2239;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTGTCT 18
DB 98 CTGGCCCGTCAGTCT 115

RESULT 31
US-09-620-312D-688/c
Sequence 688, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_pl_genes Version 1.0
SEQ ID NO 688
LENGTH: 2529
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (169) .. (1134)
US-09-620-312D-688

Query Match 77.9%; Score 14.8; DB 4; Length 2529;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTGGCCATCAGTCTCT 18
DB 1433 CTGGCCAGCAGCTGCTCT 1416

RESULT 32

US-08-311-731A-132/c
Sequence 132, Application US/08311731A
Patent No. 6583266

GENERAL INFORMATION:

APPLICANT: SMITH, DOUGLAS

APPLICANT: MAO, JEN-I

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 411

CORRESPONDENCE ADDRESS:

ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.

STREET: 600 ATLANTIC AVENUE

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/311,731A

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: GATES, EDWARD R.

REGISTRATION NUMBER: 31,616

REFERENCE/DOCKET NUMBER: C0044/7125

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/720-3500

TELEFAX: 617/720-2441

INFORMATION FOR SEQ ID NO: 132:

SEQUENCE CHARACTERISTICS:

LENGTH: 36412 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: MYCOBACTERIUM LEPRAE

US-08-311-731A-132

Query Match 77.9%; Score 14.8; DB 4; Length 36412;

Best Local Similarity 88.9%; Pred. No. 2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 TGGGCCATCAGTCTCTG 19

DB 11540 TGGGCCATCATTGCGCTG 11523

RESULT 33

US-08-742-023-15

Sequence 15, Application US/08742023

Patent No. 5800997

GENERAL INFORMATION:

APPLICANT: Beck, James J.

TITLE OF INVENTION: Detection of Maize Fungal Pathogens

TITLE OF INVENTION: Using the Polymerase Chain Reaction

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/742,023

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8587

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "primer JB586"

US-08-742-023-15

Query Match 75.8%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 1.2e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 GGCCATCAGTCTCTG 19

DB 2 GGCCATCAGTCTCTG 17

RESULT 34

US-08-968-505-15

Sequence 15, Application US/08968505

Patent No. 6071698

GENERAL INFORMATION:

APPLICANT: Beck, James J.

TITLE OF INVENTION: Detection of Maize Fungal Pathogens

TITLE OF INVENTION: Using the Polymerase Chain Reaction

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 520 White Plains Road, P.O. Box 2005

CITY: Tarrytown

STATE: NY

COUNTRY: USA

ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/968,505

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/742,023

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8587

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 15;
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer JB586"
US-08-968-505-15

Query Match 75.8%; Score 14.4; DB 3; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCATCAGTCTCTG 19
||| ||||| |||||
DB 2 GGCAATCAGTCTCTG 17

RESULT 35

US-09-016-434-481
Sequence 481, Application US/09016434
Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 481:

SEQUENCE CHARACTERISTICS:

LENGTH: 264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: UTRSN0T02
CLONE: 2260261
US-09-016-434-481

Query Match 75.8%; Score 14.4; DB 4; Length 264;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCATCAGTCTCTG 19
||| ||||| ||||| |||||

DB 38 GGCCATCAGTGCCCTG 53

RESULT 36

US-09-404-879A-327/c
Sequence 327, Application US/09404879A
Patent No. 6468546

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404, 879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for windows Version 3.0
SEQ ID NO 327
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
US-09-404-879A-327

Query Match 75.8%; Score 14.4; DB 4; Length 321;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCATCAGTCTCTG 19
||| ||||| ||||| |||||

DB 210 GGCCATCAGTGCCCTG 195

RESULT 37

US-09-620-312D-769/c
Sequence 769, Application US/09620312D
Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungting
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Fillinghast
APPLICANT: Dirmanc, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0
SEQ ID NO 769
LENGTH: 1071
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (120)..(890)

US-09-620-312D-769

Query Match 75.8%; Score 14.4; DB 4; Length 1071;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGGCATCAGTGTCTG 19
|||||
Db 498 GGCCATCAGGGCTCTG 483

RESULT 38
US-09-198-452A-6823
; Sequence 6823, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:

; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6823
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6823

Query Match 74.7%; Score 14.2; DB 4; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTGTCTG 19
|||||
Db 1 CTGACCATAAGTACTCTG 19

RESULT 39

US-09-461-697-114/c
; Sequence 114, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 132
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-114

Query Match 74.7%; Score 14.2; DB 3; Length 132;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTGTCTG 19
|||||
Db 40 CTGAGTCATCAGGGCTCTG 22

RESULT 40

US-09-461-697-112/c
; Sequence 112, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 141
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-112

Query Match 74.7%; Score 14.2; DB 3; Length 141;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTGTCTG 19
|||||
Db 49 CTGAGTCATCAGGGCTCTG 31

Search completed: January 13, 2004, 17:58:45
Job time : 47.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: January 13, 2004, 15:53:18 ; Search time 123.5 Seconds
(without alignments)
415.298 Million cell updates/sec

Title: US-09-719-737-18
Perfect score: 19
Sequence: 1 ctgggccatcagtcgtctcg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 19Jun03:*

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3:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
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11:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
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22:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	AAZ57602	Antisense oligonuc
2	19	100.0	19	ABX12695	Human CCR3 recepto
3	19	100.0	1068	AAZ1266	Human low adenosin
4	19	100.0	1068	AAA35144	Human adenosine re
5	19	100.0	1068	AB197977	Non-endogenous hum
6	19	100.0	1068	ABA94340	Human CC chemokine
7	19	100.0	1068	AAZ25222	Human chemokine (C
8	19	100.0	1071	AAZ79096	Human CCR3 chemok

C	9	19	100.0	1116	17	AAZ1336	CC-chemokine recep
C	10	19	100.0	1116	19	AAV07404	Human C-C chemokin
C	11	19	100.0	1193	17	AAZ1335	CC-chemokine recep
C	12	19	100.0	1193	19	AAV07403	Human C-C chemokin
C	13	19	100.0	1201	21	AAZ1267	Human low adenosin
C	14	19	100.0	1201	21	AAA35145	Human adenosine re
C	15	19	100.0	1201	24	ABK84282	Human cDNA differe
C	16	19	100.0	1201	25	ACA56487	Human signalling p
C	17	19	100.0	1201	25	ABZ42635	Human C-C chemokin
C	18	19	100.0	1689	17	AAZ1334	CC-chemokine recep
C	19	19	100.0	1689	18	AAZ58783	Human C-C chemokin
C	20	19	100.0	1689	19	AAV07402	Human low adenosin
C	21	19	100.0	1689	21	AAZ1268	Human C-C chemokin
C	22	19	100.0	1689	21	AAA35146	Human C-C chemokin
C	23	19	100.0	1689	24	ABL40462	Human C-C chemokin
C	24	19	100.0	1689	25	ABX13645	Human cDNA encodin
C	25	19	100.0	1717	24	ABL67066	Thyroid cancer rel
C	26	19	100.0	1717	24	AAZ25221	Human chemokine (C
C	27	19	100.0	1717	24	AAZ25245	Human chemokine (C
C	28	19	100.0	1915	18	AAZ85162	Human chemokine re
C	29	19	100.0	3426	24	ABW04010	Human ovary specif
C	30	19	100.0	3958	21	AAZ1269	Human low adenosin
C	31	19	100.0	3958	21	AAA35147	Human eosinophil e
C	32	19	100.0	5099	18	AAZ93601	Human eosinophil e
C	33	19	100.0	5791	25	ABZ68879	Nucleotide sequenc
C	34	17.4	91.6	549	22	ABA63970	Human foetal liver
C	35	17.4	91.6	549	22	ABA31145	Probe #9611 for ge
C	36	17.4	91.6	549	22	AAK12471	Human brain expres
C	37	17.4	91.6	549	22	AAK38179	Human bone marrow
C	38	17.4	91.6	549	22	AAI18973	Probe #8906 for ge
C	39	17.4	91.6	549	22	AAI44108	Probe #12794 used
C	40	17.4	91.6	549	23	ABS37802	Human liver single
C	41	17.4	91.6	549	24	ABS12213	Human genome-deriv
C	42	17.4	91.6	1565	22	AAZ86115	APEX-2 cDNA. Mus
C	43	17.4	91.6	3728	22	AAH89968	Human bone marrow
C	44	16.4	86.3	625	22	AAH31539	Human olfactory re
C	45	15.8	83.2	45	16	AAO95044	Human hippocampal

ALIGNMENTS

RESULT 1	AAZ57602	standard; DNA; 19 BP.
ID	AAZ57602	standard; DNA; 19 BP.
XX		
AC	AAZ57602;	
XX		
DT	28-MAR-2000	(first entry)
XX		
DE	Antisense oligonucleotide CCR3AS to inhibit CCR3 receptor expression.	
XX		
KW	Antisense oligonucleotide; CCR3 receptor; chemokine receptor; asthma;	
KW	allergy; cancer; receptor expression inhibitor; hypereosinophilia;	
KW	inflammation; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9966037-A2.	
XX		
PD	23-DEC-1999.	
XX		
PF	17-JUN-1999;	99WO-CA00572.
XX		
PR	17-JUN-1998;	98CA-2235420.
XX		
PA	(REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.	
XX		
PI	Renzi P;	
XX		
DR	WPI; 2000-097743/08.	
XX		
PT	Antisense oligonucleotides directed to CCR3, interleukin or granulocyte	

PT macrophage colony stimulating factor receptors, used for treating or
PT preventing asthma, allergies, hypereosinophilia, inflammation or cancer
PS Claim 5; Page 32; 72pp; English.
XX
XX This is an antisense oligonucleotide directed against the CCR3 receptor.
CC The antisense oligonucleotide inhibits CCR3 receptor expression. The CCR3
CC receptor is important in the recruitment of eosinophils into the sites of
CC allergic or asthmatic inflammation. The chemokines Botaxin, MCP-4 and
CC RANTES mediate most of their effects through the CCR3 receptor. The
CC invention relates to antisense oligonucleotides directed against a
CC nucleic acid sequence encoding either a CCR3 receptor, a common subunit
CC of interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC oligonucleotides can be used in the treatment or prevention of asthma,
CC allergy, hypereosinophilia, general inflammation or cancer.
XX
SQ Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 other;

Query Match 100.0%; Score 19; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGCCATCAGTGTCTG 19
Db 1 CTGGGCCATCAGTGTCTG 19

RESULT 2
ID ABX12695 standard; DNA; 19 BP.

XX AC ABX12695;
DT 10-MAY-2003 (first entry)

XX DE Human CCR3 receptor DNA, antisense oligonucleotide #1.

XX Human; inflammation; 2'-diaminopurine; DAP; antisense therapy;
KW DAP-modified oligonucleotide; pulmonary disease; respiratory disease;
KW neurological disease; cardiovascular disease; rheumatological disease;
KW digestive disease; cutaneous disease; ophthalmological disease;
KW urinary system disease; pathogen infection; genetic disease; cancer;
KW airway; nose; pulmonary fibrosis; adult respiratory distress syndrome;
KW cystic fibrosis; chronic obstructive lung disease; chronic bronchitis;
KW eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis;
KW hypereosinophilia; cardiac; ophthalmological; cytostatic;
KW antiasthmatic; antiallergic; antiinflammatory; immunosuppressive;
KW atopic disease; neoplastic cell proliferation; antisense;
KW CCR3 receptor; ss.

XX OS Homo sapiens.
XX PN WO2003004511-A2.

XX PD 16-JAN-2003.

XX PF 08-JUL-2002; 2002WO-CA01046.

XX PR 06-JUL-2001; 2001US-303071P.

XX PA (TOPI-) TOPIGEN PHARM INC.

XX PI Renzi P, Allam M, Allakhverdi Z;

XX DR WPI; 2003-247944/24.

XX PT Increasing in vivo efficacy of a nucleic acid molecule that is
PT administered to a mammal for inhibiting inflammation in mammals,
PT involves incorporating into the nucleic acid molecule at least one
PT nucleotide substitute -
XX

PS Claim 28; Page 11; 63pp; English.

XX The present invention relates to a method for increasing the in vivo
CC efficacy of oligonucleotides and inhibiting inflammation. The
CC oligonucleotides comprise at least one nucleotide substitute of
CC 2'-diaminopurine (DAP) and/or its analogue. The DAP nucleotide
CC substitutions are useful for increasing in vivo efficacy of a nucleic
CC acid molecule that is administered to a mammal. The DAP-modified
CC oligonucleotides are useful in antisense therapy for treating and/or
CC preventing pulmonary/respiratory diseases, neurological diseases,
CC cardiovascular diseases, rheumatological diseases, digestive diseases,
CC cutaneous diseases, ophthalmological diseases, urinary system diseases,
CC pathogen infections, genetic diseases, general inflammation and
CC cancers. The respiratory system disease is a sickness associated with
CC an inflammation of the lungs, the airways and/or the nose. The
CC respiratory system disease is selected from pulmonary fibrosis, adult
CC respiratory distress syndrome, cystic fibrosis, chronic obstructive
CC lung disease, chronic bronchitis, eosinophilic bronchitis, asthma,
CC allergy, allergic rhinitis, sinusitis and hypereosinophilia. The
CC DAP-modified oligonucleotides are more stable in the body, more
CC effective, and less toxic than standard antisense oligonucleotides.
CC DAP or its analogues are more effective than other substitutes of
CC adenosine. ABX12681-ABX12698 represent antisense oligonucleotides
CC for treating or preventing atopic diseases and neoplastic cell
CC proliferation.
XX
SQ Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 other;

Query Match 100.0%; Score 19; DB 25; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGCCATCAGTGTCTG 19
Db 1 CTGGGCCATCAGTGTCTG 19

RESULT 3
ID AAF21266/c standard; DNA; 1068 BP.

XX AC AAF21266;
DT 14-MAR-2001 (first entry)

XX DE Human low adenosine antisense oligonucleotide related sequence #2833.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW surfactant hypoproduction; pulmonary obstruction; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

XX OS Homo sapiens.
XX PN WO200062736-A2.

XX PD 26-OCT-2000.

XX PF 24-MAR-2000; 2000WO-US08020.

XX PR 06-APR-1999; 99US-0127958.

XX PA (UYEC-) UNIV EAST CAROLINA.

XX PA (NYCE/) NYCE J W.

XX PI Nyce JW;
XX

DR WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
XX Disclosure; Page 1182; 1592pp; English.
PS
XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 1068 BP; 231 A; 289 C; 243 G; 305 T; 0 other;
XX
Query Match 100.0%; Score 19; DB 21; Length 1068;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTGTCTTG 19
Db 105 CTGGGCCATCAGTGTCTTG 87
|||||
RESULT 4
AAA35144/c
ID AAA35144 standard; DNA; 1068 BP.
XX
XX AAA35144;
AC
XX
XX 28-JUL-2000 (first entry)
DT
XX
XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:18.
DE
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cystostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
KM
XX
XX Homo sapiens.
OS
XX
XX WO200009525-A2.
PN
XX
XX 24-FEB-2000.
PD

XX
XX 03-AUG-1999; 99WO-US17712.
PF
XX
XX 03-AUG-1998; 98US-0095212.
PR
XX
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX
XX Nyce JW;
PI
XX
XX WPI; 2000-205971/18.
DR
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
XX Disclosure; Page 1102; 1343pp; English.
PS
XX
XX The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
SQ Sequence 1068 BP; 231 A; 289 C; 243 G; 305 T; 0 other;
XX
Query Match 100.0%; Score 19; DB 21; Length 1068;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTGTCTTG 19
Db 105 CTGGGCCATCAGTGTCTTG 87
|||||
RESULT 5
ABI97977/c
ID ABI97977 standard; cDNA; 1068 BP.
XX
XX ABI97977;
AC
XX
XX 18-FEB-2002 (first entry)
DT
XX
XX Non-endogenous human GPCR cDNA, SEQ ID NO: 474.
DE
XX
XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW constitutively activated GPCR; agonist; disease; ss.
KM
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
OS
XX
XX WO200177172-A2.
PN
XX
XX

PD 18-OCT-2001.
XX
XX 05-APR-2001; 2001WO-US11098.
XX 07-APR-2000; 2000US-195747P.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Lehmann-Brinnsma K, Liaw CW, Lin I;
XX
XX WPI; 2001-648759/74.
XX P-PSDB; ABB56341.
XX
XX
XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with
PT versions of GPCRs -
XX
XX Example 2; Page 275; 394pp; English.
XX
XX The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous
CC constitutively activated versions of known GPCRs are used in the
CC invention for the direct identification of candidate compounds as
CC receptor agonists, inverse agonists or partial agonists. Such
CC agonists are useful as therapeutic agents for diseases or disorders
CC associated with GPCRs. The present sequence encodes a non-endogenous
CC version of a known human GPCR.
XX
XX Sequence 1068 BP; 232 A; 288 C; 244 G; 304 T; 0 other;

Query Match 100.0%; Score 19; DB 23; Length 1068;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGCCATCAGTCTCTG 19
Db 105 CTGGGCCATCAGTCTCTG 87

RESULT 6
ABA94340/c
ID ABA94340 standard; DNA; 1068 BP.

XX ABA94340;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human CC chemokine receptor 3 (CCR3) encoding DNA.
DE
XX
XX CC chemokine receptor-3; CCR3; antiallergic; antiinflammatory; human;
KW antiasthmatic; ophthalmological; dermatological; immunosuppressive;
KW antipruritic; ds.
XX
XX
XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 1..1068
FT /*tag= a
FT /product= "CCR3"
FT
FT
FT

XX WO200192520-A1.

XX 06-DEC-2001.

XX 31-MAY-2001; 2001WO-EP06195.

XX 01-JUN-2000; 2000GB-0013345.

XX (GLAX) GLAXO GROUP LTD.

XX Barnes AA, Fraser NJ, O'Shaughnessy CT, Wise A;

XX WPI; 2002-114347/15.

DR P-PSDB; ABB07240.
XX
XX Modified CC chemokine receptor-3 useful for identifying modulators of
PT eotaxin-mediated CCR3 receptor for treating allergic and inflammatory
PT disorders, comprises modifications to stabilize or enhance surface
PT expression -
XX
XX Disclosure; Page 25-26; 29pp; English.

XX
XX The invention relates to a CC chemokine receptor-3 (CCR3) modified to
CC stabilize or enhance expression of the receptor in a cell membrane.
CC Assays for investigating properties of the CCR3 receptor are useful for
CC the identification of modulators of eotaxin-mediated CCR3 receptor
CC activity. The identified modulators are useful in the treatment of
CC prophylaxis of allergic or inflammatory disorders which are responsive to
CC regulation of CCR3 receptor activity. The agents are also useful in the
CC treatment of allergy or asthma as well as ophthalmological, inflammatory,
CC gastrointestinal, dermatological, respiratory or pruritic disorders. The
CC agents are useful for treating conjunctivitis, inflammatory bowel disease,
CC eczema, allergic rhinitis, nasal polypsis, atopic dermatitis and
CC pruritis, chronic obstructive pulmonary disease (COPD) and other lung
CC disorders and immune disease. The present sequence represents the human
CC CCR3 receptor encoding DNA.
XX
XX Sequence 1068 BP; 231 A; 289 C; 243 G; 305 T; 0 other;

Query Match 100.0%; Score 19; DB 24; Length 1068;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGCCATCAGTCTCTG 19
Db 105 CTGGGCCATCAGTCTCTG 87

RESULT 7
AAD25222/c
ID AAD25222 standard; cDNA; 1068 BP.

XX AAD25222;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human chemokine (C-C motif) receptor 3 (CCR3) cDNA.
DE
XX
XX Human; chemokine (C-C motif) receptor 3; CCR3 gene; haplotyping;
KW genotyping; type IV hypersensitivity reaction; HIV-1; gene therapy;
KW human immunodeficiency virus 1; single nucleotide polymorphism; SNP;
KW chromosome 3p21.3; ss.
XX
XX
XX Homo sapiens.

XX Key Location/Qualifiers
FH variation replace (51, C)
FT /*tag= a
FT /standard name= "Single nucleotide polymorphism (SNP)"
FT /note= "Polymorphic site (PS) 3"

FT CDS 1..1068
FT /*tag= b
FT /product= "Human CCR3 protein"
FT variation replace (1052, C)
FT /*tag= c
FT /standard name= "Single nucleotide polymorphism (SNP)"
FT /note= "Polymorphic site (PS) 4"

XX WO200187908-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-US16278.

XX 18-MAY-2000; 2000US-205191P.

PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Kazemi A, Koshy B;
XX
DR WPI; 2002-055681/07.
DR P-PSDB; AAE15320.
XX
PT Isolated polymorphic variants of chemokine (C-C motif) receptor 3
PT (CCR3) gene useful for studying function of CCR3, expressing the CCR3
PT protein and to screen drugs to treat CCR3 activity-related diseases -
XX
PS Claim 25a; Fig 2; 53pp; English.
XX
CC The invention relates to genetic variants of human chemokine (C-C motif)
CC receptor 3 (CCR3) gene. The invention also relates to compositions and
CC methods for haplotyping and/or genotyping the CCR3 gene in an individual.
CC Polynucleotides of the invention are useful for studying the expression
CC and function of CCR3 and in expressing CCR3 proteins for use in screening
CC candidate drugs to treat diseases related to CCR3 activity. They are also
CC used in gene therapy. The polymorphism and haplotype data is useful for
CC validating whether CCR3 is a suitable target for drugs to treat type IV
CC hypersensitivity reactions and human immunodeficiency virus (HIV)-1,
CC screening for such drugs and reducing bias cells in clinical trials of
CC such drugs. The genotyping method is useful for determining whether an
CC individual has one haplotype or haplotype pairs. The haplotyping method
CC is useful for improving the efficiency and outcome of several steps in
CC the discovery and development of drugs for treating diseases associated
CC with CCR3 activity such as type IV hypersensitivity reactions and HIV-1.
CC The present sequence is human CCR3 cDNA. The CCR3 gene is located on
CC chromosome 3p21.3.
XX
SQ Sequence 1068 BP; 231 A; 289 C; 243 G; 305 T; 0 other;
Query Match 100.0%; Score 19; DB 24; Length 1068;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTGTCTTG 19
DB 105 CTGGGCCATCAGTGTCTTG 87
RESULT 8
AAT79096/c
ID AAT79096 standard; cDNA; 1071 BP.
XX
AC AAT79096;
XX
DT 13-MAR-1998 (first entry)
XX
DE Human CCR3 chemokine receptor coding sequence.
XX
KW CCF18 chemokine; mouse; primer; PCR; amplification; antagonist; human;
KW abnormal physiology; development; anti-viral; probe; hybridisation; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1071
FT /*tag= a
FT /product= CCR3 chemokine receptor
XX
XX WO9721812-A2.
XX PD 19-JUN-1997.
XX PF 05-DEC-1996; 96WO-US19139.
XX PR 08-DEC-1995; 95US-0567882.
XX PA (SCHE) SCHERING CORP.
XX PI Dairaghi DJ, Hara T, Miyajima A, Schall TJ, Wang W;

PI Yoshimura A;
XX
DR WPI; 1997-332784/30.
DR P-PSDB; AAW25943.
XX
PT New isolated chemokine CCF8 and chemokine receptor CCR3 - used to
PT develop products useful for the diagnosis and treatment of
PT conditions associated with abnormal physiology or development
XX
PS Claim 15; Page 60-62; 73pp; English.
XX
CC This is the nucleotide sequence encoding a novel CCR3 chemokine
CC receptor isolated from a Th0-activated human T-cell cDNA library
CC using the sequence amplified by primers AAT79097 and AAT79098 as a
CC probe. The encoded protein can be used to screen for (ant)agonists that
CC bind to the novel CCF18 chemokines (AAW25941 and AAW25942). These
CC (ant)agonists are useful in the treatment of conditions associated with
CC abnormal physiology or development.
XX
SQ Sequence 1071 BP; 231 A; 292 C; 242 G; 306 T; 0 other;
Query Match 100.0%; Score 19; DB 18; Length 1071;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTGTCTTG 19
DB 105 CTGGGCCATCAGTGTCTTG 87
RESULT 9
AAT31336/c
ID AAT31336 standard; DNA; 1116 BP.
XX
AC AAT31336;
XX
DT 15-NOV-1996 (first entry)
XX
DE CC-chemokine receptor 3 consensus DNA sequence.
XX
KW CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;
KW antiinflammatory; eosinophil; ds.
XX
OS Homo sapiens.
XX
PN WO9622371-A2.
XX
PD 25-JUL-1996.
XX
PF 19-JAN-1996; 96WO-US00608.
XX
PR 19-JAN-1995; 95US-0375199.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (LEUK-) LEUKOSITE INC.
XX
PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
PI Qin S;
XX
DR WPI; 1996-354528/35.
DR P-PSDB; AAW03378.
XX
PT Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
XX
PS Claim 1; Page 114-115; 153pp; English.
XX
CC A consensus DNA sequence (AAT31336) codes for a novel human receptor
CC (AAW03378), designated Eos L2 or C-C chemokine receptor 2 (CCR-3).
CC It was deduced by comparing a genomic clone (AAT31334) and a cDNA
CC clone (AAT31335) coding for CCR-3 proteins (AAW03376 and AAW03377)

CC having slightly different sequences. Initial sequence information
CC revealed 2 regions in which the cDNA sequence appeared to be shifted in
CC frame, resulting in 2 sets of 4 contiguous amino acid differences
CC in the predicted proteins. Further sequence analysis revealed only
CC a single difference between the 2 open reading frames, the genomic
CC clone coding for threonine at position 276 and the cDNA clone for
CC serine.

XX
SQ Sequence 1116 BP; 246 A; 286 C; 257 G; 306 T; 21 other;

Query Match 100.0%; Score 19; DB 17; Length 1116;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
|||
Db 119 CTGGGCCATCAGTCTCTG 101

RESULT 10
AAV07404/c
ID AAV07404 standard; DNA; 1116 BP.
XX
AC AAV07404;
XX
DT 28-SEP-1998 (first entry)
XX
DE Human C-C chemokine receptor 3 consensus nucleic acid.
XX
KM C-C chemokine receptor 3; CKR-3; CCR3; Eos L2; human;
KM G protein-coupled receptor; leukocyte; antibody; antagonist;
KM inflammation; allergy; asthma; graft rejection; infection;
KM autoimmune disease; drug screening; therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 15..1082
FT /*tag= a
FT
XX
PN WO9814480-A1.
XX
PD 09-APR-1998.
XX
PF 24-SEP-1997; 97WO-US17103.
XX
PR 30-SEP-1996; 96US-0720565.
XX
PA (LEUK-) LEUKOSITE INC.
XX
PI Mackay CR, Ponath PD;
XX
DR WPI; 1998-286418/25.
DR P-PSDB; AAW51746.
XX
PT Antibodies to chemokine receptor-3 protein - useful for diagnosis
PT and treatment of inflammatory conditions, e.g. allergy, asthma,
PT autoimmune disease, graft rejection or cancer
XX
PS Disclosure; Page 137-138; 185pp; English.

XX This is a consensus sequence constructed by alignment of a genomic
CC DNA sequence (see AAV07402) and a cDNA clone (see AAV07403) coding for
CC novel human C-C chemokine receptor 3, also designated CKR-3, CCR3
CC or Eos L2, that binds and mediates chemotaxis in response to
CC chemokines such as eotaxin, RANTES and MCP-3. Sequence comparison
CC revealed 2 regions in the cDNA sequence that appeared to be shifted
CC in frame, resulting from an insertion of a base followed by the
CC deletion of a base, or the deletion of a base followed by the
CC insertion of a base. These alterations resulted in 4 contiguous
CC amino acid differences in the predicted proteins (see AAW51744 and
CC AAW51745) at positions 263-266 and 276-279, respectively. In
CC addition, the genomic clone codes for threonine (ACG) at

CC position 276 and the cDNA clone for serine (AGC). The predicted
CC amino acid sequence from the consensus is given in AAW51747.
CC CKR-3 nucleic acids, polypeptides, antibodies, agonists and
CC antagonists are useful for diagnosis and treatment of
CC inflammatory conditions, autoimmune diseases and infections.
XX
SQ Sequence 1116 BP; 246 A; 287 C; 257 G; 306 T; 20 other;

Query Match 100.0%; Score 19; DB 19; Length 1116;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
|||
Db 119 CTGGGCCATCAGTCTCTG 101

RESULT 11
AAT31335/c
ID AAT31335 standard; cDNA; 1193 BP.
XX
AC AAT31335;
XX
DT 15-NOV-1996 (first entry)
XX
DE CC-chemokine receptor 3 cDNA clone.
XX
KM CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;
KM antiinflammatory; eosinophil; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 92..1159
FT /*tag= a
FT variation 918..919
FT /*tag= b
FT /note= "CKR-3 cDNA clone has GC at positions
FT 918-919, coding for serine (AGC) at
FT position 276; a genomic clone has CG at
FT these positions, coding for threonine
FT (AGC)"
XX
PN WO9622371-A2.
XX
PD 25-JUL-1996.
XX
PF 19-JAN-1996; 96WO-US00608.
XX
PR 19-JAN-1995; 95US-0375199.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (LEUK-) LEUKOSITE INC.
XX
PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
PI Qin S;
XX
DR WPI; 1996-354528/35.
DR P-PSDB; AAW03377.
XX
PT Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
XX
PS Claim 1; Page 111-113; 153pp; English.

XX A genomic DNA clone (AAT31335) codes for a novel receptor (AAW03377),
CC designated Eos L2 or C-C chemokine receptor 3 (CKR-3), involved
CC in leukocyte migration associated with inflammation. It was
CC isolated from a human library constructed from eosinophils obtd.
CC from a patient with hyper-eosinophilic syndrome using a probe
CC (p4 cDNA) encoding the MIP-1alpha/RANTES receptor. A CKR-3

CC genomic clone (AAT31334) was also isolated, and a consensus sequence
CC is given in AAT31336. The cDNA and genomic clones can be used for
CC the prodn. of recombinant CKR-3 in host cells, or to design
CC antisense sequences useful for treating inflammatory disease.
XX
SQ Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 other;

Query Match 100.0%; Score 19; DB 17; Length 1193;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGCCATCAGTCTCTG 19
Db 196 CTGGGCCATCAGTCTCTG 178
|||||

RESULT 12
AAV07403/c
ID AAV07403 standard; cDNA; 1193 BP.
XX
AC AAV07403;
XX
DT 28-SEP-1998 (first entry)
XX
DE Human C-C chemokine receptor 3 cDNA.
XX
KW C-C chemokine receptor 3; CKR-3; CCR3; Eos L2; human;
KW G protein-coupled receptor; leukocyte; antibody; antagonist;
KW inflammation; allergy; asthma; graft rejection; infection;
KW autoimmune disease; drug screening; therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 92..1159
FT /*tag= a
XX
XX
PN WO9814480-A1.
XX
PD 09-APR-1998.
XX
PF 24-SEP-1997; 97WO-US17103.
XX
PR 30-SEP-1996; 96US-0720565.
XX
PA (LEUK-) LEUKOSITE INC.
XX
PI Mackay CR, Ponath PD;
XX
DR WPI; 1998-286418/25.
DR P-PSDB; AAW51745.
XX
XX
PT Antibodies to chemokine receptor-3 protein - useful for diagnosis
PT and treatment of inflammatory conditions, e.g. allergy, asthma,
PT autoimmune disease, graft rejection or cancer
XX
XX
PS Example 8; Page 134-136; 185pp; English.
XX
CC This cDNA codes for novel human C-C chemokine receptor 3 (see
CC AAW51745), also designated CKR-3, CCR3 or Eos L2, that binds and
CC mediates chemotaxis in response to chemokines such as eotaxin,
CC RANTES and MCP-3. The cDNA was isolated from a human eosinophil
CC cDNA library constructed from eosinophils obtained from a patient
CC with hypereosinophilic syndrome, and using CKR-1 cDNA as probe. A
CC genomic DNA sequence (see AAV07402) is also provided as well as a
CC consensus sequence (see AAV07404) for CKR-3. The invention relates
CC to isolated and/or recombinant nucleic acids encoding CKR-3,
CC isolated or recombinant CKR-3 polypeptides, recombinant nucleic
CC acid constructs, host cells useful for production of recombinant
CC CKR-3 proteins, to antibodies reactive with the receptors, and to
CC methods of using these products to identify ligands, antagonists
CC and agonists of receptor function. Inhibitors of CKR-3 can be used
CC to treat: inflammatory or allergic diseases and conditions,

CC including respiratory allergic diseases such as asthma, allergic
CC rhinitis, hypersensitivity lung disease, hypersensitivity
CC pneumonia, eosinophilic pneumonia (e.g. Loeffler's syndrome,
CC chronic eosinophilic pneumonia, interstitial lung disease (ILD))
CC e.g. idiopathic pulmonary fibrosis or ILD associated with
CC rheumatoid arthritis, systemic sclerosis, Sjogren's syndrome, polymyositis
CC or dermatomyositis), systemic anaphylaxis or hypersensitivity
CC responses, drug allergy, insect sting allergy, inflammatory bowel
CC disease, such as Crohn's disease and ulcerative colitis,
CC spondyloarthropathy, scleroderma, psoriasis, inflammatory
CC dermatosis such as dermatitis, eczema, atopic dermatitis,
CC allergic contact dermatitis, urticaria, vasculitis (e.g. necrotizing,
CC cutaneous and hypersensitivity vasculitis); eosinophilic myositis
CC and eosinophilic fasciitis; autoimmune diseases such as rheumatoid
CC arthritis, psoriatic arthritis, multiple sclerosis, systemic lupus
CC erythematosus, myasthenia gravis, juvenile onset diabetes,
CC glomerulonephritis, autoimmune thyroiditis and Behcet's disease;
CC graft rejection, including allograft rejection or graft-versus-host
CC disease; cancers with leukocyte infiltration of the skin or organs;
CC and also reperfusion injury, atherosclerosis, certain hematologic
CC malignancies, septic shock and endotoxic shock. Promoters of CKR-3
CC function can be used for treating: immunosuppression e.g. in AIDS
CC patients or individuals undergoing radiation therapy, chemotherapy,
CC therapy for autoimmune disease or other drug therapy, and
CC immunosuppression due congenital deficiency in receptor function or
CC other causes; and infectious diseases such as parasitic diseases,
CC including helminth infections, such as nematodes (round worms).
XX
XX The agents can also be used for detection and diagnosis.
XX
SQ Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 other;

Query Match 100.0%; Score 19; DB 19; Length 1193;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGCCATCAGTCTCTG 19
Db 196 CTGGGCCATCAGTCTCTG 178
|||||

RESULT 13
AAF21267/c
ID AAF21267 standard; DNA; 1201 BP.
XX
AC AAF21267;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2834.
XX
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.
XX
XX NYce JW;
PI
XX WPI; 2000-679539/66.
DR
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
XX Disclosure; Page 1182-1183; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, such as stimulating factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
XX Sequence 1201 BP; 278 A; 320 C; 267 G; 336 T; 0 other;
SQ
Query Match 100.0%; Score 19; DB 21; Length 1201;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTCTCTG 19
Db 136 CTGGGCCATCAGTCTCTG 118
RESULT 14
AAA35145/c
ID AAA35145 standard; DNA; 1201 BP.
XX
XX AAA35145;
AC
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:19.
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KM phosphorothioate; impaired respiration; inflammation; allergy;
KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KM antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
XX Homo sapiens.

XX
XX WO200009525-A2.
PN
XX
XX 24-FEB-2000.
PD
XX
XX 03-AUG-1999; 99WO-US17712.
PF
XX
XX 03-AUG-1998; 98US-0095212.
PR
XX
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX
XX NYce JW;
PI
XX
XX WPI; 2000-205971/18.
DR
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
XX Disclosure; Page 1102; 1343pp; English.
PS
XX
XX The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing the
CC bronchoconstriction and inflammation. AAA3213 to AAA3512 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
XX Sequence 1201 BP; 278 A; 320 C; 267 G; 336 T; 0 other;
SQ
Query Match 100.0%; Score 19; DB 21; Length 1201;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTCTCTG 19
Db 136 CTGGGCCATCAGTCTCTG 118
RESULT 15
ABK84282/c
ID ABK84282 standard; cDNA; 1201 BP.
XX
XX ABK84282;
AC
XX
XX 14-AUG-2002 (first entry)
DT
XX
DE Human cDNA differentially expressed in granulocytic cells #853.
XX
XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
KM viral infection; parasitic infection; protozoal infection;
KM fungal infection; sterile inflammatory disease; psoriasis;
KM rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
XX
XX

KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN WO200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30821.
XX
PR 03-OCT-2000; 2000US-237189P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
PS Claim 1; SEQ ID NO 853; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1201 BP; 278 A; 320 C; 267 G; 336 T; 0 other;

Query Match 100.0%; Score 19; DB 24; Length 1201;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTGCTCTG 19
|||||

DB 136 CTGGGCCATCAGTGCTCTG 118
RESULT 16
ID ACA56487/c
XX ACA56487 standard; cDNA; 1201 BP.
XX
AC ACA56487;
XX
DT 06-JUN-2003 (first entry)
XX
DE Human signalling pathway polynucleotide probe SEQ ID NO 1085.
XX
KW Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS Homo sapiens.
XX
PN US6500938-B1.
XX
PD 31-DEC-2002.
XX
PF 30-JAN-1998; 98US-0016434.
XX
PR 30-JAN-1998; 98US-0016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX
DR WPI; 2003-352189/33.
XX
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides -
XX
PS Claim 1; SEQ ID NO 1085; 65pp; English.
XX
CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=06500938B1.
XX
SQ Sequence 1201 BP; 278 A; 320 C; 267 G; 336 T; 0 other;

Query Match 100.0%; Score 19; DB 25; Length 1201;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTGCTCTG 19
|||||

DB 136 CTGGGCCATCAGTGCTCTG 118

RESULT 17
ABZ42635/c
ID ABZ42635 standard; DNA; 1201 BP.
XX
XX
AC ABZ42635;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human C-C chemokine receptor 3 nucleotide SEQ ID NO:63.
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KM G protein-coupled receptor modulator; antibody; immune-related disease;
KM growth-related disease; cell regeneration-related disease; AIDS; cancer;
KM immunological-related cell proliferative disease; autoimmune disease;
KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KM ulcer; gene; ds.
XX
XX Homo sapiens.
OS
XX WO200261087-A2.
PN
XX 08-AUG-2002.
PD
XX 19-DEC-2001; 2001WO-US50107.
PF
XX 19-DEC-2000; 2000US-257144P.
PR
XX 19-DEC-2000; 2000US-257144P.
XX
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
PA
XX Burner GC, Roush CL, Brown JP;
PI
XX WPI; 2003-046718/04.
XX P-PSDB; ABP81791.
DR
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -
XX
XX
XX Disclosure; Fig 1; 523pp; English.
PS
XX
XX The present invention describes antigenic peptides (I) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
CC an antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.
XX
XX Sequence 1201 BP; 278 A; 320 C; 267 G; 336 T; 0 other;
,SQ

Query Match 100.0%; Score 19; DB 25; Length 1201;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTGTCTG 19
DB 136 CTGGGCCATCAGTGTCTG 118
RESULT 18
AAT31334/c
ID AAT31334 standard; DNA; 1689 BP.
XX
XX AAT31334;
AC
XX 15-NOV-1996 (first entry)
DT
XX CC-chemokine receptor 3 genomic DNA.
DE
XX CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;
KM antiinflammatory; eosinophil; ds.
KM
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 181..1248
FT /*tag= a
FT 1007..1008
FT variation /*tag= b
FT /note= "CKR-3 genomic clone has CG at positions
FT 1007-1008, coding for threonine (ACG) at
FT position 276; a cDNA clone has GC at
FT these positions, coding for serine (AGC)"
FT misc_difference 1291
FT /*tag= C
FT /note= "base n at position 1291 is not identified
FT in the specification"
XX
XX WO9622371-A2.
PN
XX 25-JUL-1996.
PD
XX 19-JAN-1996; 96WO-US00608.
PF
XX 19-JAN-1995; 95US-0375199.
PR
XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (LEUK-) LEUKOSITE INC.
XX
XX Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
PI Qin S;
XX
XX WPI; 1996-354528/35.
XX P-PSDB; AAW03376.
DR
XX
XX Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
PT
XX
XX Claim 1; Page 109; 153pp; English.
PS
XX A genomic DNA clone (T31334) codes for a novel receptor (W03376),
XX designated Eos L2 or C-C chemokine receptor 3 (CKR-3), involved
XX in leukocyte migration associated with inflammation. It was
XX isolated from a human genomic library in EMBL3 SP7/T7 vector by
XX screening with a PCR fragment generated from eosinophil cDNA
XX using degenerate primers (see also T31337-44). A CKR-3 cDNA
XX clone (T31335) was also isolated, and a consensus sequence is
XX given in T31336. The genomic and cDNA clones can be used for
XX the prodn. of recombinant CKR-3 in host cells, or to design
XX antisense sequences useful for treating inflammatory disease.
CC

XX SQ Sequence 1689 BP; 431 A; 416 C; 344 G; 497 T; 1 other;
Query Match 100.0%; Score 19; DB 17; Length 1689;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCATCAGTCTCTG 19
|||
Db 285 CTGGGCATCAGTCTCTG 267
RESULT 19
AAT58783/c
ID AAT58783 standard; DNA; 1689 BP.
XX AC AAT58783;
XX DT 30-SEP-1997 (first entry)
XX DE Human C-C chemokine receptor 3 DNA.
XX KW Human; eotaxin; eosinophil; chemoattractant; stimulation;
KW accumulation; attraction; chemotaxis; diagnosis; prevention;
KW treatment; disease; inflammation; allergy; asthma; rhinitis;
KW hypersensitivity; lung; pneumonia; Loeffler's; syndrome;
KW interstitial; ILD; idiopathic pulmonary fibrosis;
KW rheumatoid arthritis; systemic; lupus erythematosus; SLE;
KW ankylosing spondylitis; sclerosis; Sjorgen's; polymyositis;
KW dermatomyositis; bowel; anaphylaxis; drug; penicillin;
KW cephalosporin; insect sting; Crohn's; ulcerative colitis;
KW spondyloarthritis; scleroderma; psoriasis; dermatosis;
KW dermatitis; eczema; atopic; urticaria; necrotising; cutaneous;
KW vasculitis; myositis; fascitis; multiple sclerosis;
KW myasthenia gravis; juvenile onset diabetes; glomerulonephritis;
KW autoimmune; thyroiditis; Bechet's; graft; rejection;
KW transplantation; allograft; graft versus host; cancer;
KW leukocyte infiltration; reperfusion injury; atherosclerosis;
KW haematologic malignancy; septic; endotoxic; shock;
KW polymyositis; dermatomyositis; immunosuppression; immunodeficiency;
KW AIDS; radiation therapy; chemotherapy; autoimmune; corticosteroid;
KW C-C chemokine receptor 3; CRK3; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 181..1248
FT /*tag= a
FT /product= CRK3
XX PN WO9700960-A1.
XX PD 09-JAN-1997.
XX PF 21-JUN-1996; 96WO-US10723.
XX PR 23-JUN-1995; 95US-0494093.
XX PA (LEUK-) LEUKOSITE INC.
XX PI Mackay C, Newman W, Ponath PD, Qin S, Ringler DJ;
XX WPI; 1997-087387/08.
XX DR P-PSDB; AAW10100.
XX PT New isolated human eotaxin gene - used to develop prods. for the
PT diagnosis and treatment of e.g. inflammation, allergies, auto-immune
PT disease, infections and tumours
XX PS Example 7; Page 97; 130pp; English.
XX CC The present sequence encodes human C-C chemokine receptor 3 (CRK3),
CC to which human eotaxin (he), an eosinophil specific chemoattractant

CC capable of stimulating eosinophil accumulation and/or attracting
CC eosinophils (including chemotaxis), binds.
CC he can be used to develop products for the diagnosis, prevention or
CC treatment of he associated diseases or conditions. The products can
CC be used to treat inflammatory or allergic diseases and conditions,
CC including respiratory allergic diseases (e.g. asthma, allergic
CC rhinitis, hypersensitivity lung diseases or pneumonitis,
CC eosinophilic pneumonias such as Loeffler's syndrome and chronic
CC eosinophilic pneumonia, interstitial lung diseases (ILD) such as
CC idiopathic pulmonary fibrosis or ILD associated with rheumatoid
CC arthritis, systemic lupus erythematosus (SLE), ankylosing
CC spondylitis, systemic sclerosis, Sjorgen's syndrome, polymyositis
CC or dermatomyositis), systemic anaphylaxis or hypersensitivity
CC responses, drug allergies (e.g. to penicillin and cephalosporins),
CC insect sting allergies, inflammatory bowel diseases (e.g. Crohn's
CC disease and ulcerative colitis), spondyloarthritis,
CC scleroderma, psoriasis and inflammatory dermatoses (e.g.
CC dermatitis, eczema, atopic dermatitis, allergic contact dermatitis,
CC urticaria and necrotising, cutaneous and hypersensitivity
CC vasculitis), eosinophilic myositis and fascitis, multiple
CC sclerosis, SLE, myasthenia gravis, juvenile onset diabetes,
CC glomerulonephritis, autoimmune thyroiditis, Bechet's disease, graft
CC rejection (e.g. in transplantation) including allograft rejection or
CC graft versus host disease and cancers with leukocyte infiltration
CC of the skin or organs. The products can also be used to treat other
CC diseases or conditions requiring the inhibition of undesirable
CC inflammatory responses, including reperfusion injury,
CC atherosclerosis, certain haematologic malignancies, cytokine
CC induced toxicity (e.g. septic or endotoxic shock), polymyositis,
CC dermatomyositis, immunosuppression (e.g. in individuals with
CC immunodeficiency syndromes such as AIDS, undergoing radiation
CC therapy, chemotherapy, therapy for autoimmune disease or other drug
CC therapy, such as corticosteroid therapy, which causes
CC immunosuppression), immunosuppression due to (e.g. congenital)
CC deficiency (e.g. in eotaxin) or infectious diseases such as parasitic
CC diseases.
CC Degenerate primers based on the guinea pig eotaxin amino acid
CC sequence were used for the reverse transcriptase polymerase chain
CC reaction (RT-PCR) amplification of RNA isolated from inflamed,
CC eosinophilic lung tissue obtained from Balb/c mice sensitised to
CC ovalbumin. The amplification product was used as a probe to screen
CC a human genomic library in vector EMBL3 SP6/T7 to obtain the he
CC gene.
XX SQ Sequence 1689 BP; 431 A; 416 C; 344 G; 497 T; 1 other;
XX FH Key Location/Qualifiers
XX FT CDS 181..1248
XX FT /*tag= a
XX FT /product= CRK3
XX PN WO9700960-A1.
XX PD 09-JAN-1997.
XX PF 21-JUN-1996; 96WO-US10723.
XX PR 23-JUN-1995; 95US-0494093.
XX PA (LEUK-) LEUKOSITE INC.
XX PI Mackay C, Newman W, Ponath PD, Qin S, Ringler DJ;
XX WPI; 1997-087387/08.
XX DR P-PSDB; AAW10100.
XX PT New isolated human eotaxin gene - used to develop prods. for the
PT diagnosis and treatment of e.g. inflammation, allergies, auto-immune
PT disease, infections and tumours
XX PS Example 7; Page 97; 130pp; English.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 181..1248
XX FT /*tag= a
XX FT /product= CRK3
XX PN WO9700960-A1.
XX PD 09-JAN-1997.
XX PF 21-JUN-1996; 96WO-US10723.
XX PR 23-JUN-1995; 95US-0494093.
XX PA (LEUK-) LEUKOSITE INC.
XX PI Mackay C, Newman W, Ponath PD, Qin S, Ringler DJ;
XX WPI; 1997-087387/08.
XX DR P-PSDB; AAW10100.
XX PT New isolated human eotaxin gene - used to develop prods. for the
PT diagnosis and treatment of e.g. inflammation, allergies, auto-immune
PT disease, infections and tumours
XX PS Example 7; Page 97; 130pp; English.
XX CC The present sequence encodes human C-C chemokine receptor 3 (CRK3),
CC to which human eotaxin (he), an eosinophil specific chemoattractant

FT CDS 181..1248
/*tag= a
XX WO9814480-A1.
XX PD 09-APR-1998.
XX PF 24-SEP-1997; 97WO-US17103.
XX PR 30-SEP-1996; 96US-0720565.
XX (LEUK-) LEUKOSITE INC.
XX PA Mackay CR, Ponath PD;
XX PI WPI; 1998-286418/25.
XX DR P-PSDB; AAW51744.
XX
PT Antibodies to chemokine receptor-3 protein - useful for diagnosis
PT and treatment of inflammatory conditions, e.g. allergy, asthma,
PT autoimmune disease, graft rejection or cancer
XX
XX Example 2; Fig 1A-C; 185pp; English.
XX
CC This genomic DNA codes for novel human C-C chemokine receptor 3
CC (see AAW51744), also designated CKR-3, CCR3 or Eos I2, that binds and
CC mediates chemotaxis in response to chemokines such as eotaxin,
CC RANTES and MCP-3. The DNA was isolated from a human genomic phage
CC library using as probe a PCR fragment that had been generated from
CC eosinophil cDNA using primers (see AAV07405-12) based on known
CC chemokine receptor genes. A cDNA clone (see AAV07403) for CKR-3 is
CC also provided. Comparison of the sequences suggests that the
CC genomic DNA has an intron that separates the promoter and most
CC of the 5' untranslated region from the coding region. A consensus
CC of the genomic and cDNA sequences is provided (see AAV07404). The
CC invention relates to isolated and/or recombinant nucleic acids
CC encoding CKR-3, isolated or recombinant CKR-3 polypeptides,
CC recombinant nucleic acid constructs, host cells useful for
CC production of recombinant CKR-3 proteins, to antibodies reactive
CC with the receptors, and to methods of using these products to
CC identify ligands, antagonists and agonists of receptor function.
CC Inhibitors of CKR-3 can be used to treat: inflammatory or allergic
CC diseases and conditions, including respiratory allergic diseases
CC such as asthma, allergic rhinitis, hypersensitivity lung disease,
CC hypersensitivity pneumonitis, eosinophilic pneumonia (e.g.
CC Loeffler's syndrome, chronic eosinophilic pneumonia, interstitial
CC lung disease (ILD) e.g. idiopathic pulmonary fibrosis or ILD
CC associated with rheumatoid arthritis, systemic lupus erythematosus,
CC ankylosing spondylitis, systemic sclerosis, Sjogren's syndrome,
CC polymyositis or dermatomyositis), systemic anaphylaxis or
CC hypersensitivity responses, drug allergy, insect sting allergy,
CC inflammatory bowel disease, such as Crohn's disease and ulcerative
CC colitis, spondyloarthropathy, scleroderma, psoriasis, inflammatory
CC dermatosis such as dermatitis, eczema, atopic dermatitis,
CC allergic contact dermatitis, urticaria, vasculitis (e.g. necrotizing,
CC cutaneous and hypersensitivity vasculitis); eosinophilic myositis
CC and eosinophilic fasciitis; autoimmune diseases such as rheumatoid
CC arthritis, psoriatic arthritis, multiple sclerosis, systemic lupus
CC erythematosus, myasthenia gravis, juvenile onset diabetes,
CC glomerulonephritis, autoimmune thyroiditis and Behcet's disease;
CC graft rejection, including allograft rejection or graft-versus-host
CC disease; cancers with leukocyte infiltration of the skin or organs;
CC and also reperfusion injury, atherosclerosis, certain haematologic
CC malignancies, septic shock and endotoxic shock. Promoters of CKR-3
CC function can be used for treating: immunosuppression e.g. in AIDS
CC patients or individuals undergoing radiation therapy, chemotherapy,
CC therapy for autoimmune disease or other drug therapy, and
CC immunosuppression due congenital deficiency in receptor function or
CC other causes; and infectious diseases such as parasitic diseases,
CC including helminth infections, such as nematodes (round worms).
XX The agents can also be used for detection and diagnosis.
XX
XX Sequence 1689 BP; 431 A; 416 C; 344 G; 497 T; 1 other;
XX ,SQ

Query Match 100.0%; Score 19; DB 19; Length 1689;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCATCAGTCTCTG 19
Db 285 CTGGGCATCAGTCTCTG 267
RESULT 21
AAAF21268/c
ID AAF21268 standard; DNA; 1689 BP.
XX
XX AAF21268;
AC
XX
DT 14-MAR-2001 (first entry)
XX
XX
DE Human low adenosine antisense oligonucleotide related sequence #2835.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200062736-A2.
XX PD 26-OCT-2000.
XX PF 24-MAR-2000; 2000WO-US08020.
XX PR 06-APR-1999; 99US-0127958.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX PA (NYCE/) NYCE J W.
XX PI Nyce JW;
XX DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
XX Disclosure; Page 1183; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense
XX oligonucleotides and compositions (I) comprising them. In the antisense
XX oligonucleotides the A is replaced by a 'universal' or alternative base.
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
XX immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
XX The antisense oligonucleotides and (I) can be used to down-regulate the
XX expression and or activity of target polypeptides associated with
XX lung/respiratory disorders and malignancies, such as stimulating and
XX activating peptide factors and transmitters, transcription factors,
XX immunoglobulins and antibodies, antibody receptors, cytokines and
XX chemokines, endogenously produced specific and non-specific enzymes,
XX binding proteins, adhesion molecules and their receptors, cytokine and
XX chemokine receptors, adenosine receptors, bradykinin receptors, central
XX nervous system (CNS) and peripheral nervous and non-nervous system
XX receptors, CNS and peripheral nervous and non-nervous system peptide
XX transmitters, defensins, growth factors, vasoactive peptides and
XX receptors, binding proteins and malignancy associated proteins. The
XX antisense oligonucleotides may be used in this way to treat disorders
XX including respiratory obstruction (especially pulmonary obstruction

CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.

XX
SQ Sequence 1689 BP; 430 A; 416 C; 345 G; 497 T; 1 other;

Query Match 100.0%; Score 19; DB 21; Length 1689;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTGTCTCTG 19
DB 285 CTGGGCCATCAGTGTCTCTG 267

RESULT 22
AAA35146/c
ID AAA35146 standard; DNA; 1689 BP.
XX
AC AAA35146;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:20.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 1103; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cyostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,

CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 185, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.

XX
SQ Sequence 1689 BP; 430 A; 416 C; 345 G; 497 T; 1 other;

Query Match 100.0%; Score 19; DB 21; Length 1689;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTGTCTCTG 19
DB 285 CTGGGCCATCAGTGTCTCTG 267

RESULT 23
ABL40462/c
ID ABL40462 standard; cDNA; 1689 BP.
XX
AC ABL40462;
XX
DT 10-JUN-2002 (first entry)
XX
DE Human C-C chemokine receptor 3 (CCR3) protein encoding cDNA.
XX
KW Mucosae-associated epithelial chemokine; MEC; C-C chemokine receptor;
KW CCR3; CCR10; anti-inflammatory; cyostatic; immunomodulator; anti-viral;
KW antibacterial; chemokine; human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 181..1248
FT /*tag= a
FT /product= "CCR3"
XX
PN WO200214532-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25734.
XX
PR 15-AUG-2000; 2000US-0638914.
XX
PA (MILL-) MILLENNIUM PHARM INC.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Butcher EC, Kunkel EJ, Pan J, Soler-Ferran D;
XX
DR WPI; 2002-269204/31.
DR P-PSDB; ABB07733.
XX
PT Identifying modulators of mucosae-associated epithelial chemokine (MEC)
PT receptors 3 or 10 (CCR3/10), useful for treating inflammatory diseases,
PT comprises detecting formation of MEC-CCR3/10 complex or modulation of a
PT MEC-induced response -
XX
PS Example 2; Fig 4A-B; 92pp; English.
XX
CC The invention relates to identifying agents that inhibit or promote the

binding or a mammalian mucosae-associated epithelial chemokine (MEC) to a mammalian C-C chemokine receptor 3 (CCR3) or 10 (CCR10). The method involves: (a) detecting or measuring the formation of a complex between the MEC, and the CCR3 or CCR10; or (b) determining the ability of the test agent to inhibit or augment a MEC-induced response. An augmentation of complex formation, relative to a control, is indicative that the agent is a promoter. The method is useful for identifying modulators (e.g. inhibitors or promoter) of MEC-induced functions of CCR3 and/or CCR10. The inhibitors are useful for treating inflammatory diseases or conditions in a subject, e.g. oral inflammatory condition (e.g. Sjogren's syndrome or Behcet's syndrome), mastitis, chronic obstructive lung disease, asthma, inflammatory bowel disease (e.g. Crohn's disease, ulcerative colitis or celiac disease), IGA nephropathy or dermatitis herpetiformis. The promoters are useful for treating cancers (e.g. solid tumours or cutaneous T cell lymphoma), neoplastic disease, retinopathy, macular degeneration, bacterial infections, tuberculous leprosy, viral infections, AIDS, neutropenias or bronchiectasis. The present sequence represents the human CCR3 protein encoding cDNA.

SQ Sequence 1689 BP; 430 A; 416 C; 345 G; 497 T; 1 other;

Query Match	100.0%;	Score 19;	DB 24;	Length 1689;
-------------	---------	-----------	--------	--------------

Best Local Similarity 100.0%; Pred. No. 6.2;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 CTGGCCATCAGTGTCTG 19
         |||||
Db     285 CTGGCCATCAGTGTCTG 267
```

RESULT 24
ABX13645/

ID ABX13645 standard; cDNA; 1689 BP.

AC ABX13645;

DT 12-FEB-2003 (first entry)

DE Human cDNA encoding C-C chemokine receptor 3, CCR3.

KW Human, ss; gene; mucosae-associated epithelial chemokine; MEC;
KW chromosome 5; C-C chemokine receptor; CCR3; CCR10; allergy;
KW Iga antibody-secreting cell; inflammatory disease; Sjogren's syndrome;
KW oral inflammatory condition; Behcet's syndrome; mastitis;
KW chronic obstructive lung disease; asthma; inflammatory bowel disease;
KW Iga nephropathy; dermatitis herpetiformis; ulcerative colitis;
KW coeliac disease; autoimmune disease; arthritis; multiple sclerosis;
KW systemic lupus erythematosus; myasthenia gravis; diabetes;
KW autoimmune thyroiditis; graft rejection; atherosclerosis; cancer;
KW infectious disease; immunosuppression.

OS Homo sapiens.

FH	key	Location/Qualifiers
FT	CDS	181..1248

PN US2002137107-A1.

PD 26-SEP-2002.

PF 15-AUG-2001; 2001US-0931381.

PR 15-AUG-2000; 2000US-0638914.

PA (MILL-) MILLENNIUM PHARM INC.

PI Butcher EC, Kunkel EJ, Pan J, Soler-Ferran D;

DR WPI; 2003-102382/09.

DR P-PSDB; ABG72634.

XX

PT Identifying agents that inhibit or promote binding of mammalian MEC to
PT CCR3 or CCR10, useful for treating an inflammatory and autoimmune
PT diseases, atherosclerosis, cancers, infectious diseases, diabetes,
PT arthritis and asthma -

PS Disclosure; Fig 4; 46pp; English.

1 The invention relates to identifying an agent which inhibits or promotes
2 the binding of mammalian MEC (mucosae-associated epithelial chemokine) to
3 a mammalian C-C chemokine receptor 3 (CCR3) or CCR10 comprising:
4 (a) combining an agent to be tested, a composition comprising a
5 naturally occurring mammalian CCR3, CCR10 or MEC-binding variant, and a
6 mammalian MEC; and (b) detecting or measuring the formation of a complex
7 between the MEC and the CCR3, CCR10 or MEC-binding variant. The
8 method alternatively comprises: (a) combining an agent to be tested, a
9 cell expressing a protein comprising a naturally occurring mammalian
10 CCR3, CCR10 or MEC-binding variant, and a mammalian MEC under conditions
11 suitable for detecting an MEC-induced response; and (b) determining the
12 ability of the test agent to inhibit or augment, where inhibition or
13 augmentation of a MEC-induced response by the agent indicates that the
14 agent is an inhibitor or promoter. Also included are: (1) an
15 immunoglobulin or antigen-binding fragment which binds a naturally
16 occurring mammalian CCR3 or CCR10, and inhibits the binding of a
17 naturally occurring mammalian MEC to the receptor; and (2) modulating the
18 activity of an IGA antibody-secreting cell in a subject, comprising
19 administering MEC or an agent that promotes or inhibits the binding of
20 MEC to CCR3 and/or CCR10. The methods and compositions of the present
21 invention are useful for treating an inflammatory disease or allergic
22 condition such as oral inflammatory condition (e.g., Sjogren's or
23 Behcet's syndrome), mastitis, chronic obstructive lung disease, asthma,
24 inflammatory bowel disease, IGA nephropathy, dermatitis herpetiformis,
25 ulcerative colitis and coeliac disease. They can also be used in
26 autoimmune diseases such as arthritis, multiple sclerosis,
27 systemic lupus erythematosus, myasthenia gravis, diabetes and autoimmune
28 thyroiditis, graft rejection, atherosclerosis, cancers, infectious
29 diseases and immunosuppression (many other diseases and disorders are
30 listed in the specification). The gene for MEC is located on chromosome
31 5. The present sequence is the Human cDNA encoding C-C chemokine
32 receptor 3, CCR3.

SQ Sequence 1689 BP; 430 A; 416 C; 345 G; 497 T; 1 other;

Query Match	100.0%;	Score 19;	DB 25;	Length 1689;
-------------	---------	-----------	--------	--------------

Best Local Similarity 100.0%; Pred. No. 6.2;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTGGCCATCAGTCTTG	19
Db	285	CTGGCCATCAGTCTTG	267

RESULT 25
ABL67066/

ID	ABL67066 standard; DNA; 1717 BP.
----	----------------------------------

AC ABL67066;

DT 15-MAY-2002 (first entry)

DE Thyroid cancer related gene sequence SEQ ID NO:5403.

KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.

Homo sapiens.

PN WO200194629-A2.

PD 13-DEC-2001.

PF 30-MAY-2001; 2001WO-US10838.

XX 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Sopet DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
DR
XX
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX
PS Claim 1; SEQ ID 5403; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine

CC carcinoma, papillary carcinoma and Wilms's tumour.
XX
SQ Sequence 1717 BP; 434 A; 428 C; 351 G; 504 T; 0 other;
Query Match 100.0%; Score 19; DB 24; Length 1717;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGCCATCAGTGCTCTG 19
|||||
Db 309 CTGGCCATCAGTGCTCTG 291
RESULT 26
AAD25221/c
ID AAD25221 standard; DNA; 1717 BP.
XX
AC AAD25221;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human chemokine (C-C motif) receptor 3 (CCR3) gene #1.
XX
KW Human; chemokine (C-C motif) receptor 3; CCR3 gene; haplotyping;
KW genotyping; type IV hypersensitivity reaction; HIV-1; gene therapy;
KW human immunodeficiency virus 1; single nucleotide polymorphism; SNP;
KW Chromosome 3p21.3; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace (92, T)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT replace (197, A)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT CDS 205..1272
FT /*tag= c
FT /product= "Human CCR3 protein"
FT /note= "This region corresponds to exon 1"
FT variation replace (255, C)
FT /*tag= d
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT replace (1256, C)
FT /*tag= e
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200187908-A2.
XX
XX 22-NOV-2001.
PD
XX 18-MAY-2001; 2001WO-US16278.
PF
XX 18-MAY-2000; 2000US-205191P.
PR
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Choi JY, Kazemi A, Koshy B;
PI
XX WPI; 2002-055681/07.
DR P-PSDB; AA15320.
XX
XX Isolated polymorphic variants of chemokine (C-C motif) receptor 3
PT (CCR3) gene useful for studying function of CCR3, expressing the CCR3
PT protein and to screen drugs to treat CCR3 activity-related diseases -
XX
XX Example 1; Fig 1; 53pp; English.
XX
XX The invention relates to genetic variants of human chemokine (C-C motif)
CC receptor 3 (CCR3) gene. The invention also relates to compositions and
CC methods for haplotyping and/or genotyping the CCR3 gene in an individual.
CC Polynucleotides of the invention are useful for studying the expression

CC and function of CCR3 and in expressing CCR3 proteins for use in screening
CC candidate drugs to treat diseases related to CCR3 activity. They are also
CC used in gene therapy. The polymorphism and haplotype data is useful for
CC validating whether CCR3 is a suitable target for drugs to treat type IV
CC hypersensitivity reactions and human immunodeficiency virus (HIV)-1,
CC screening for such drugs and reducing bias cells in clinical trials of
CC such drugs. The genotyping method is useful for determining whether an
CC individual has one haplotype or haplotype pairs. The haplotyping method
CC is useful for improving the efficiency and outcome of several steps in
CC the discovery and development of drugs for treating diseases associated
CC with CCR3 activity such as type IV hypersensitivity reactions and HIV-1.
CC The present sequence is human CCR3 gene located on chromosome 3p21.3.
XX
SQ Sequence 1717 BP; 434 A; 428 C; 351 G; 504 T; 0 other;

Query Match 100.0%; Score 19; DB 24; Length 1717;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGCCATCAGTGTCTTG 19
|||
Db 309 CTGGGCCATCAGTGTCTTG 291

RESULT 27
AAD25245/C
ID AAD25245 standard; DNA; 1717 BP.

XX AAD25245;
XX
DT 12-MAR-2002 (first entry)

DE Human chemokine (C-C motif) receptor 3 (CCR3) gene #2.

XX Human; chemokine (C-C motif) receptor 3; CCR3 gene; haplotyping;
KW genotyping; type IV hypersensitivity reaction; HIV-1; gene therapy;
KW human immunodeficiency virus 1; polymorphism; chromosome 3p21.3; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FH misc_feature 92

FT /*tag= a
FT /note= "This degenerate base represents polymorphic
FT site (PS) 1"
PT 197

FT /*tag= b
FT /note= "This degenerate base represents polymorphic
FT site (PS) 2"
PT 255

FT /*tag= c
FT /note= "This degenerate base represents polymorphic
FT site (PS) 3"
PT 1256

FT /*tag= d
FT /note= "This degenerate base represents polymorphic
FT site (PS) 4"

XX WO200187908-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-US16278.

XX 18-MAY-2000; 2000US-205191P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Choi JY, Kazemi A, Koshy B;

XX WPI; 2002-055681/07.

XX Isolated polymorphic variants of chemokine (C-C motif) receptor 3

PT (CCR3) gene useful for studying function of CCR3, expressing the CCR3
PT protein and to screen drugs to treat CCR3 activity-related diseases -
XX
PS Claim 5, Page 53; 53pp; English.

XX The invention relates to genetic variants of human chemokine (C-C motif)
CC receptor 3 (CCR3) gene. The invention also relates to compositions and
CC methods for haplotyping and/or genotyping the CCR3 gene in an individual.
CC Polynucleotides of the invention are useful for studying the expression
CC and function of CCR3 and in expressing CCR3 proteins for use in screening
CC candidate drugs to treat diseases related to CCR3 activity. They are also
CC used in gene therapy. The polymorphism and haplotype data is useful for
CC validating whether CCR3 is a suitable target for drugs to treat type IV
CC hypersensitivity reactions and human immunodeficiency virus (HIV)-1,
CC screening for such drugs and reducing bias cells in clinical trials of
CC such drugs. The genotyping method is useful for determining whether an
CC individual has one haplotype or haplotype pairs. The haplotyping method
CC is useful for improving the efficiency and outcome of several steps in
CC the discovery and development of drugs for treating diseases associated
CC with CCR3 activity such as type IV hypersensitivity reactions and HIV-1.
CC The present sequence is human CCR3 gene located on chromosome 3p21.3.
XX
SQ Sequence 1717 BP; 434 A; 427 C; 350 G; 502 T; 4 other;

Query Match 100.0%; Score 19; DB 24; Length 1717;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGCCATCAGTGTCTTG 19
|||
Db 309 CTGGGCCATCAGTGTCTTG 291

RESULT 28
AAT85162/C
ID AAT85162 standard; cDNA; 1915 BP.

XX AAT85162;

XX 14-DEC-1997 (first entry)

DE Human chemokine receptor 88-2B cDNA.

XX Chemokine receptor 88-2B; atherosclerosis; rheumatoid arthritis;
KW tumour; asthma; viral infection; AIDS; inflammation;
KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
KW G protein coupled receptor; human; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 362..1429
FT /*tag= a

XX WO9722698-A2.

XX 26-JUN-1997.

XX 20-DEC-1996; 96WO-US20759.

XX 07-JUN-1996; 96US-0661393.

XX 20-DEC-1995; 95US-0575967.

XX (ICOS-) ICOS CORP.

XX Gray PW, Raport CJ, Schweickart VL;

XX WPI; 1997-341689/31.

XX P-PSDB; AAW27124.

XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used
PT to modulate leukocyte trafficking, e.g. for treatment of
PT inflammation, tumours, viral infections, autoimmune diseases, etc.

XX Claim 7; Page 48-50; 65pp; English.
PS
XX
CC This sequence comprises a full-length cDNA coding for novel human
CC chemokine receptor 88-2B (AAW27124), a G protein coupled receptor that
CC is involved in leukocyte trafficking. The 88-2B cDNA was obtained
CC from a macrophage cDNA library using 88-2B-specific primers. A
CC full-length clone (see AAT89161) for chemokine receptor 88C (AAW27123)
CC was also obtained. 88C and 88-2B cDNAs can be used to produce
CC recombinant polypeptides in transformed host cells for use in the
CC treatment of e.g. atherosclerosis, rheumatoid arthritis, tumours,
CC asthma, viral infection, AIDS and inflammatory conditions. Nucleic
CC acid fragments can be used to isolate genomic sequences, to detect
CC alleles of the gene (for diagnosis or in gene therapy), to alter
CC receptor genetics to facilitate identification of modulators and to
CC produce knockout animals, and (antisense forms) to alter/study the
CC genetics and expression of the receptor.
XX
SQ Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 other;

Query Match 100.0%; Score 19; DB 18; Length 1915;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
DB 466 CTGGGCCATCAGTCTCTG 448

RESULT 29
ABT04010/c
ID ABT04010 standard; DNA; 3426 BP.
XX
XX AC ABT04010;
XX
DT 25-SEP-2002 (first entry)
XX
XX Human ovary specific coding sequence SEQ ID NO: 29.
DE
XX Human; ovary; ovarian cancer; ovarian disease; gene therapy; gene;
KM cyostatic; ds.
XX
XX Homo sapiens.
OS
XX WO200240720-A2.
PN
XX 23-MAY-2002.
PD
XX 20-NOV-2001; 2001WO-US45010.
PF
XX 20-NOV-2000; 2000US-249997P.
PR
XX (DIAD-) DIADEXUS INC.
PA
XX Salceda S, Macina RA, Recipon H, Caffery R, Sun Y, Liu C;
PI WPI; 2002-547588/58.
DR
XX New ovary polypeptides useful for detecting, diagnosing, monitoring,
PT treating, staging and imaging cancers in humans having cancer and
PT non-cancerous ovary disease -
XX
XX Claim 1; Page 162-164; 296pp; English.
XX
CC The present invention provides human proteins and coding sequences
CC specifically found in ovary cells. These can be used in the diagnosis and
CC treatment of ovarian diseases, including cancer. The present sequence is
CC a coding sequence of the invention.
XX
SQ Sequence 3426 BP; 1107 A; 828 C; 714 G; 777 T; 0 other;

Query Match 100.0%; Score 19; DB 24; Length 3426;
Best Local Similarity 100.0%; Pred. No. 6.9;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTCTCTG 19
DB 234 CTGGGCCATCAGTCTCTG 216

RESULT 30
AAF21269/c
ID AAF21269 standard; DNA; 3958 BP.
XX
XX AAF21269;
AC
XX 14-MAR-2001 (first entry)
DT
XX
DE Human low adenosine antisense oligonucleotide related sequence #2836.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; BS.
XX
XX Homo sapiens.
OS
XX WO200062736-A2.
PN
XX 26-OCT-2000.
PD
XX 24-MAR-2000; 2000WO-US08020.
PF
XX 06-APR-1999; 99US-0127958.
PR
XX (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
XX Nyce JW;
PI
XX WPI; 2000-679539/66.
DR
XX
XX Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
XX Disclosure; Page 1183-1184; 1592pp; English.
PS
XX
XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cyostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,

CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 3958 BP, 939 A; 1025 C; 855 G; 1138 T; 1 other;
Query Match 100.0%; Score 19; DB 21; Length 3958;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTCTCTG 19
Db 2554 CTGGGCCATCAGTCTCTG 2536
RESULT 31
AAA35147/c standard; DNA; 3958 BP.
XX AAA35147;
AC
XX 28-VUL-2000 (first entry)
DT
XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:21.
DE
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
XX Homo sapiens.
OS
XX WO200009525-A2.
PN
XX 24-FEB-2000.
PD
XX 03-AUG-1999; 99WO-US17712.
PF
XX 03-AUG-1998; 98US-0095212.
PR
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX
PI Nyce JW;
XX
XX WPI; 2000-205971/18.
DR
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers
XX
XX Disclosure; Page 1103-1104; 1343pp; English.
PS
XX
XX The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,

CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing the
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC given in the sequence listing.
XX
SQ Sequence 3958 BP; 939 A; 1025 C; 855 G; 1138 T; 1 other;
Query Match 100.0%; Score 19; DB 21; Length 3958;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTCTCTG 19
Db 2554 CTGGGCCATCAGTCTCTG 2536
RESULT 32
AAT93601/c standard; cDNA; 5099 BP.
XX AAT93601;
AC
XX 07-MAY-1998 (first entry)
DT
XX Human eosinophil eotaxin receptor CC CKR3 encoding cDNA.
DE
XX Eosinophil eotaxin receptor; CC CKR3; human; treatment; dermatitis;
KW atopic condition; allergic rhinitis; conjunctivitis; bronchial asthma;
KW beta-chemokine receptor; viral infection; ss.
XX
XX Homo sapiens.
OS
XX
XX Key location/Qualifiers
FH 1.3586
FT misc_feature /*tag= a
FT /note= "5' genomic DNA flanking sequence"
FT CDS 3587..4654
FT /*tag= b
FT /product= "human eosinophil eotaxin receptor"
FT misc_feature 4655..5099
FT /*tag= c
FT /note= "terminator region"
XX
XX
XX WO9741154-A1.
PN
XX
XX 06-NOV-1997.
PD
XX
XX 24-APR-1997; 97WO-US06568.
PF
XX 17-JAN-1997; 97GB-0000894.
PR 26-APR-1996; 96US-0016158.
PR 26-APR-1996; 96US-0017113.
XX
XX (MERI) MERCK & CO INC.
PA
XX
XX Daugherty BL, Demartino JA, Siciliano SJ, Springer MS;
PI
XX WPI; 1997-549685/50.
DR P-PSDB; AAW31850.
XX
XX New isolated human eosinophil eotaxin receptor - used to develop
PT products for treating and preventing atopic conditions e.g. allergic
PT rhinitis, dermatitis, conjunctivitis and bronchial asthma
XX

PS Claims 12, 13, 14; Pages 16-20; 51pp; English.
XX
CC This cDNA encodes a human eosinophil eotaxin receptor. This 5099 base
CC pair sequence comprises a 1065 base pair open reading frame encoding a
CC 355 amino acid eosinophil eotaxin receptor protein, flanked by a 5'
CC genomic DNA sequence and a 3' terminator region. This novel eosinophil
CC eotaxin receptor is a human beta-chemokine receptor designated CC CKR3.
CC Agents which bind to this eosinophil eotaxin receptor can be used for
CC the treatment and prevention of atopic conditions such as allergic
CC rhinitis, dermatitis, conjunctivitis and bronchial asthma. Agents which
CC block this eosinophil eotaxin receptor can be used to prevent viral
CC infection in healthy individuals and slow or halt viral progression
CC in infected patients.
XX
SQ Sequence 5099 BP; 1388 A; 1171 C; 1013 G; 1527 T; 0 other;

Query Match 100.0%; Score 19; DB 18; Length 5099;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTGCTCTG 19
DB 3691 CTGGGCCATCAGTGCTCTG 3673

RESULT 33
ABZ68879/C
ID ABZ68879 standard; cDNA; 5791 BP.
XX AC ABZ68879;
XX DT 28-MAY-2003 (first entry)
XX DE Nucleotide sequence of human chemokine receptor CCR3.
XX Human; chemokine receptor; CCR3; viral infection; surface protein;
KW respiratory virus infection; respiratory syncytial virus infection;
KW RSV infection; bronchiolitis; bronchitis; pneumonia; asthma; gene; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 4015..5082
FT /*tag= a
FT /product= "CCR3"
XX
XX PN WO2003014153-A2.
XX PD 20-FEB-2003.
XX PF 12-AUG-2002; 2002WO-CA01248.
XX PR 10-AUG-2001; 2001US-311088P.
XX PA (TOPI-) TOPIGEN PHARM INC.
XX PI Renzi P, Zemzoumi K, Lamkhioved B;
XX WPI; 2003-247991/25.
DR P-PSDB; ABP97726.
XX
PT Modulating viral infection of a cell, for treating or preventing
PT respiratory virus infections, bronchitis, pneumonia or asthma, by
PT modulating a binding interaction between a cell chemokine-receptor and
PT a surface protein of the virus -
XX
PS Disclosure; Page 84-88; 120pp; English.
XX
CC The present sequence encodes human chemokine receptor CCR3. The
CC specification describes a method for modulating viral infection of
CC a cell. the method comprises modulating a binding interaction between
CC a cell chemokine-receptor and a surface protein of the virus. The
CC proviso is that the cell chemokine-receptor is not CX3CR1 and that the

CC virus is not HIV. The method is useful for treating or preventing
CC respiratory virus infection in vertebrates, more particularly
CC respiratory syncytial virus (RSV) infections, and related diseases,
CC e.g. bronchiolitis, bronchitis, pneumonia or asthma.
XX
SQ Sequence 5791 BP; 1624 A; 1285 C; 1160 G; 1722 T; 0 other;

Query Match 100.0%; Score 19; DB 25; Length 5791;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTGCTCTG 19
DB 4119 CTGGGCCATCAGTGCTCTG 4101

RESULT 34
ABA63970/C
ID ABA63970 standard; DNA; 549 BP.
XX AC ABA63970;
XX DT 01-FEB-2002 (first entry)
XX DE Human foetal liver single exon nucleic acid probe #12275.
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
OS Homo sapiens.
XX
XX PN WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00669.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-483447/52.
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human fetal liver -
XX PS Claim 1; SEQ ID NO 12275; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 549 BP; 127 A; 148 C; 178 G; 96 T; 0 other;

Query Match 91.6%; Score 17.4; DB 22; Length 549;
Best Local Similarity 94.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGCCATCAGTGCTCTG 19
|||||

Db 101 CTGGCCATGAGTCTCTG 83

RESULT 35
ABA31145/C
ID ABA31145 standard; DNA; 549 BP.
XX
AC ABA31145;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #9611 for gene expression analysis in human heart cell sample.
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 1; SEQ ID No 9611; 530bp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 549 BP; 127 A; 148 C; 178 G; 96 T; 0 other;

Query Match 91.6%; Score 17.4; DB 22; Length 549;
Best Local Similarity 94.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
|||
Db 101 CTGGCCATGAGTCTCTG 83

RESULT 36
AAK12471/C
ID AAK12471 standard; DNA; 549 BP.
XX
AC AAK12471;

XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 12462.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 12462; 650bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 549 BP; 127 A; 148 C; 178 G; 96 T; 0 other;

Query Match 91.6%; Score 17.4; DB 22; Length 549;
Best Local Similarity 94.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
|||
Db 101 CTGGCCATGAGTCTCTG 83

RESULT 37
AAK38179/C
ID AAK38179 standard; DNA; 549 BP.
XX
AC AAK38179;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 12736.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.

```

XX 30-JAN-2001; 2001WO-US00668.
PF 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
XX Example 4; SEQ ID NO: 12736; 658bp + Sequence Listing; English.
PS
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
XX Sequence 549 BP; 127 A; 148 C; 178 G; 96 T; 0 other;
SQ
Query Match 91.6%; Score 17.4; DB 22; Length 549;
Best Local Similarity 94.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTGGGCCATCAGTGCTCTG 19
101 CTGGGCCATGAGTGCTCTG 83
DB
RESULT 38
AA118973/c
ID AA118973 standard; DNA; 549 BP.
XX
AC AA118973;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #8906 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX

```

DR	WPI; 2001-488901/53.
XX	
PT	Human genome-derived single exon nucleic acid probes useful for
PT	analyzing gene expression in human cervical epithelial cells -
XX	
PS	Claim 25; SEQ ID No 8906; 487bp; English.
XX	
CC	The present invention relates to human single exon nucleic acid probes
CC	(SENP). The present sequence is one such probe. The SENPs are derived
CC	from human HeLa cells. The SENPs can be used to produce a single exon
CC	microarray, which can be used for measuring human gene expression in a
CC	sample derived from human cervical epithelial cells. By measuring gene
CC	expression, the probes are therefore useful in grading and/or staging
CC	of diseases of the cervix, notably cervical cancer.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 549 BP; 127 A; 148 C; 178 G; 96 T; 0 other;
	Query Match 91.6%; Score 17.4; DB 22; Length 549;
	Best Local Similarity 94.7%; Pred. No. 35;
	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy	1 CTGGGCCATCAGTGTCTTG 19
Dd	101 CTGGGCCATGAGTGTCTTG 83
	RESULT 39
	AAI44108/c
ID	AAI44108 standard; DNA; 549 BP.
XX	
AC	AAI44108;
XX	
DT	17-OCT-2001 (first entry)
XX	
DE	Probe #12794 used to measure gene expression in human placenta sample.
KX	
KM	Probe; microarray; human; placenta; antenatal diagnosis;
KW	genetic disorder; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200157272-A2.
XX	
PD	09-AUG-2001.
XX	
Pf	30-JAN-2001; 2001WO-US00663.
XX	
PR	04-FEB-2000; 2000US-0180312.
PR	26-MAY-2000; 2000US-0207456.
PR	30-JUN-2000; 2000US-0608408.
PR	03-AUG-2000; 2000US-0632366.
PR	21-SEP-2000; 2000US-0234687.
PR	27-SEP-2000; 2000US-0236359.
PR	04-OCT-2000; 2000GB-0024263.
XX	
PA	(MOLE-) MOLECULAR DYNAMICS INC.
XX	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	
DR	WPI; 2001-488897/53.
XX	
PT	Human genome-derived single exon nucleic acid probes useful for
PT	analyzing gene expression in human placenta -
XX	
PS	Claim 25; SEQ ID No 12794; 654bp; English.
XX	
CC	The present invention relates to single exon nucleic acid probes (SENP).
CC	The present sequence is one such probe. The probes are useful for
CC	producing a microarray for predicting, measuring and displaying gene
CC	expression in samples derived from human placenta. The probes are useful

CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 549 BP; 127 A; 148 C; 178 G; 96 T; 0 other;

Query Match 91.6%; Score 17.4; DB 22; Length 549;
Best Local Similarity 94.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
|||
Db 101 CTGGCCATGAGTCTCTG 83

RESULT 40
ABS37802/c

ID ABS37802 standard; DNA; 549 BP.

XX AC ABS37802;

XX DT 25-FEB-2003 (first entry)

XX DE Human liver single exon probe, SEQ ID No 12792.

XX KW Human; single exon nucleic acid probe; liver; cirrhosis;
XX KM hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
XX KW coronary heart disease; ss.

XX OS Homo sapiens.

XX PN WO200157273-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US00664.

XX PR 04-FEB-2000; 2000US-0180312.

XX PR 26-MAY-2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488898/53.

XX PT Human genome-derived single exon nucleic acid probes useful for

XX PT analysing gene expression in human adult liver -

XX PS Claim 1; SEQ ID No 12792; 658bp; English.

XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX CC measuring human gene expression in a sample derived from human adult
XX CC liver, comprising one of 13109 defined nucleotide sequences given in the
XX CC specification (or complements/ fragments). The probe hybridises at high
XX CC stringency to a nucleic acid molecule expressed in the human adult
XX CC liver. (I) may be used for predicting, measuring and displaying gene
XX CC expression in samples derived from human adult liver. The genes
XX CC identified may be involved in genetic liver diseases such as cirrhosis,
XX CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
XX CC is associated with coronary heart disease. ABS25011-ABS51005 represent
XX CC human liver single exon nucleic acid probes of the invention.
XX CC Note: The sequence information for this patent does not appear in the
XX CC printed specification but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 549 BP; 127 A; 148 C; 178 G; 96 T; 0 other;

Query Match 91.6%; Score 17.4; DB 23; Length 549;
Best Local Similarity 94.7%; Pred. No. 35;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGCCATCAGTCTCTG 19
|||
Db 101 CTGGCCATGAGTCTCTG 83

Search completed: January 13, 2004, 18:02:40
Job time : 124.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2004, 15:53:18 ; Search time 1192.5 Seconds
(without alignments)
387.241 Million cell updates/sec

Title: US-09-719-737-9

Perfect score: 19
Sequence: 1 gggctgcagcgsgatggt 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inu: *
19: em_gss_pln: *
20: em_gss_vrt: *
21: em_gss_fun: *
22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rnd: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gss1: *
29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	299	10	BF884753 PM3-ET020
2	19	100.0	354	12	BM146496 BM146496
3	19	100.0	357	10	BF986303 BF986303
4	19	100.0	478	13	BU431613 BU431613

C	5	19	100.0	785	14	CB961169	CB961169	AGENCOURT
C	6	19	100.0	1031	13	BX359469	BX359469	BX359469
C	7	17.4	91.6	209	14	H31083	H31083	EST104774 R
C	8	17.4	91.6	266	10	BB306760	BB306760	BB306760
C	9	17.4	91.6	318	13	BQ331140	BQ331140	PM3-ET020
C	10	17.4	91.6	355	10	BE102744	BE102744	UI-R-BT1-
C	11	17.4	91.6	386	9	AA892154	AA892154	EST195957
C	12	17.4	91.6	463	14	CB735745	CB735745	AMGNNUC:N
C	13	17.4	91.6	573	14	CB614996	CB614996	AMGNNUC:N
C	14	17.4	91.6	580	28	AZ952841	AZ952841	2M0217N18
C	15	17.4	91.6	1077	12	BI114889	BI114889	602861478
C	16	17.4	91.6	1164	12	BQ059970	BQ059970	AGENCOURT
C	17	17.4	91.6	1562	10	BE887786	BE887786	601511359
C	18	17.4	91.6	3874	11	AK031524	AK031524	Mus muscu
C	19	17	89.5	993	29	BZ554088	BZ554088	pac61-60-
C	20	16.4	86.3	206	12	BJ239259	BJ239259	BJ239259
C	21	16.4	86.3	214	9	AW612888	AW612888	hh37g01.x
C	22	16.4	86.3	240	9	AJ460522	AJ460522	AJ460522
C	23	16.4	86.3	253	12	BJ293359	BJ293359	BJ293359
C	24	16.4	86.3	284	12	BJ299950	BJ299950	BJ299950
C	25	16.4	86.3	292	12	BJ299963	BJ299963	BJ299963
C	26	16.4	86.3	292	14	CA644225	CA644225	wreln.pk0
C	27	16.4	86.3	324	12	BI013302	BI013302	PM4-ET015
C	28	16.4	86.3	336	13	BU974641	BU974641	HB28J24r
C	29	16.4	86.3	350	14	R25769	R25769	yh43f06.r1
C	30	16.4	86.3	355	9	AW769047	AW769047	h157h11.x
C	31	16.4	86.3	362	9	AI473980	AI473980	tm04g09.x
C	32	16.4	86.3	369	10	BF112016	BF112016	7137f04.x
C	33	16.4	86.3	380	13	BQ189288	BQ189288	UI-E-EJ1-
C	34	16.4	86.3	382	9	AA613554	AA613554	nq22e02.8
C	35	16.4	86.3	394	10	BE411862	BE411862	ISC010.A0
C	36	16.4	86.3	400	12	BM443000	BM443000	EBro02_SQ
C	37	16.4	86.3	402	14	CB871117	CB871117	HC02F21y
C	38	16.4	86.3	403	28	BH306574	BH306574	CH230-192
C	39	16.4	86.3	406	9	AI492104	AI492104	tg07b01.x
C	40	16.4	86.3	413	12	BI499969	BI499969	1e12h06.x
C	41	16.4	86.3	417	13	BX103590	BX103590	BX103590
C	42	16.4	86.3	419	10	BE411823	BE411823	ISC009.F0
C	43	16.4	86.3	419	14	CB867914	CB867914	HC02F21w
C	44	16.4	86.3	420	14	CA614992	CA614992	wrl.pk149
C	45	16.4	86.3	420	14	CA614992	CA614992	wrl.pk149

ALIGNMENTS

RESULT 1
BF884753 299 bp mRNA linear EST 17-JAN-2001
PM3-ET0207-271200-003-e12 ET0207 Homo sapiens CDNA, mRNA sequence.
BF884753
BF884753.1 GI:12275402
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 299)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-ET0207-271200-003-e12&t3=2000-12-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 299.
Location/Qualifiers

FEATURES
source
1. 299
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0207"
/note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
ORIGIN
50 a 86 c 79 g 84 t

Query Match
Best Local Similarity 100.0%; Score 19; DB 10; Length 299;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCTGCAGCGGATGCT 19
|||||
Db 270 GGGTCTGCAGCGGATGCT 288

RESULT 2
BM146496 354 bp mRNA linear EST 30-NOV-2001
TCAP1E4963 Pediatric acute myelogenous leukemia cell (FAB M1)
Baylor-HGSC project=TCAP Homo sapiens cDNA clone TCAP4963, mRNA sequence.
ACCESSION
BM146496
VERSION
BM146496.1 GI:17165472
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 354)
Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr., Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F. Pediatric Leukemia cDNA Sequencing Project (2001)
TITLE
Unpublished
JOURNAL
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@tccc.org
Seq primer: M13 primer.
FEATURES
source
1. 354
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TCAP4963"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="myeloid cell"
/dev_stage="pediatric 6 years"

/lab_host="DH10B"
/clone_lib="Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAP"
/note="Vector: lambda PSB; Site_1: BamHI; Site_2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGACTCGAGCGCGCCAGAGAG(T)VN 3'; V=A,C,G, N=A,C,G,T] and then dg tailed. Second strand was primed with a BamHI-dC primer [5'AGAGAGCTCGATCCGCGCGCCGCAATATAAT(C) 3']. Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and Sali sites of lambda PSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, Sasaki, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"

BASE COUNT
ORIGIN
77 a 113 c 106 g 58 t

Query Match
Best Local Similarity 100.0%; Score 19; DB 12; Length 354;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCTGCAGCGGATGCT 19
|||||
Db 320 GGGTCTGCAGCGGATGCT 302

RESULT 3
BF986303 357 bp mRNA linear EST 23-JAN-2001
QV4-GN0144-031000-446-b10 GN0144 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF986303
VERSION
BF986303.1 GI:12392610
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-GN0144-031000-446-b10&t3=2000-10-03&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 357.
Location/Qualifiers

FEATURES
source
1. 357
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/dev stage="Adult"
 /clone lib="GN0144"
 /note="Organ: placenta normal; Vector: puc18; Site_1: SmaI
 ; Site_2: SmaI; A mini-library was made by cloning
 products derived from ORESTES PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer
 Research) profiles into the pUC 18 vector. Reverse
 transcription of tissue mRNA and cDNA amplification were
 performed under low stringency conditions."

BASE COUNT 77 a 110 c 116 g 54 t
 ORIGIN
 Query Match 100.0%; Score 19; DB 10; Length 357;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
 |||||
 Db 316 GGGTCTGCAGCGGATGCT 298

RESULT 4
 BU431613/c 478 bp mRNA linear EST 09-SEP-2002
 LOCUS UI-HF-BNO-af-r-f-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
 DEFINITION IMAGE:3067902 5', mRNA sequence.

ACCESSION BU431613.1 GI:22770100
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares lab
 cDNA Library Arrayed by: M.B. Soares lab
 DNA Sequencing by: M.B. Soares lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES

source Location/Qualifiers

1..478
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3067902"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_lines="MGC85"
 /lab_host="DH10B (LT1)"
 /clone_lib="NIH_MGC_50"
 /note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (3.5-4.4kb). Directionally cloned. Cells provided by
 Louis M. Staudt, Ph.D. Library preparation by Maria de
 Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 97 a 158 c 148 g 75 t
 ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 478;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
 |||||

Db 303 GGGTCTGCAGCGGATGCT 285

RESULT 5
 CB961169/c 785 bp mRNA linear EST 29-APR-2003
 LOCUS AGENCOURT 13762074 NIH_MGC_147 Homo sapiens cDNA clone
 DEFINITION IMAGE:30344148 5', mRNA sequence.

ACCESSION CB961169.1 GI:30217286
 VERSION CB961169
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Stefan Hansson
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
 and advice from Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDAM379 row: p column: 13
 High quality sequence stop: 651.

FEATURES

source Location/Qualifiers

1..785
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30344148"
 /tissue_type="Human Placenta"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_147"
 /note="Organ: placenta; Vector: pBluescriptR; Site 1:
 all-XhoI; Site 2: BamH; Oligo-dT primed using primer
 5'-TTTTTTTTTTTATTVN-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."

BASE COUNT 154 a 257 c 234 g 140 t
 ORIGIN

Query Match 100.0%; Score 19; DB 14; Length 785;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
 |||||
 Db 341 GGGTCTGCAGCGGATGCT 323

RESULT 6
 BX359469/c 1031 bp mRNA linear EST 05-MAY-2003
 LOCUS BX359469 Homo sapiens PLACENTA.COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0DI057H02 5-PRIME, mRNA sequence.

ACCESSION BX359469.1 GI:30382361
 VERSION BX359469
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1031)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 10421.f. For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DI057DD01QP1&cluster=10421.f. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DI057DD01QP1.

FEATURES
 source
 1. 1031
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI057YH02"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 191 a 336 c 293 g 204 t 7 others

ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 1031;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCACGGGATGCT 19
 |||||
 Db 202 GGGTCTGCACGGGATGCT 184

RESULT 7
 H31083/c 209 bp mRNA linear EST 02-APR-1998
 LOCUS H31083
 DEFINITION EST104774 Rat PC-12 cells, untreated Rattus sp. cDNA clone RPCAB19
 5' end, mRNA sequence.
 ACCESSION H31083
 VERSION H31083.1 GI:976505
 KEYWORDS EST.
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 209)
 AUTHORS Lee, N.H., Weinstein, K.G., Kirkness, E.F., Earle-Hughes, J.A., Fuldner
 , R.A., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D., Kerlavage
 , A.R., Fraser, C.M., and Venter, J.C.
 TITLE Comparative expressed-sequence-tag analysis of differential gene
 expression profiles in PC-12 cells before and after nerve growth
 factor treatment
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92, 8303-8307 (1995)
 MEDLINE 95396786
 PUBMED 7667285
 COMMENT Other_ESTs: EST104773
 Contact: Lee, NH
 The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org
 For clone availability please contact the TIGR Database
 (tcbinfo@tigr.org)
 Seq primer: M13 Reverse.

FEATURES
 source
 Location/Qualifiers
 1. 209
 /organism="Rattus sp."
 /mol_type="mRNA"
 /db_xref="AFCC (inhost):2000079"
 /db_xref="taxon:10118"
 /clone="RPCAB19"
 /clone_lib="Rat PC-12 cells, untreated"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; poly(A) + RNA was purified from untreated PC12 cells
 cultured for 9 days. cDNA was constructed using an
 oligo-dT primer and directionally cloned using the lambda
 ZAP II Vector Kit by Stratagene"

BASE COUNT 48 a 61 c 51 g 49 t

ORIGIN

Query Match 91.6%; Score 17.4; DB 14; Length 209;
 Best Local Similarity 94.7%; Pred. No. 1.7e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGCACGGGATGCT 19
 |||||
 Db 194 GGGTCTGCACGAGATGCT 176

RESULT 8
 BB306760/c 266 bp mRNA linear EST 10-JUL-2000
 LOCUS BB306760
 DEFINITION BB306760 RIKEN full-length enriched, adult male corpora
 quadrigenina Mus musculus cDNA clone B230209H01 3' similar to
 U79774 Mus musculus NNP-1 var (NNP-1) mRNA, mRNA sequence.
 BB306760
 BB306760.1 GI:9007465
 EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 266)
 REFERENCE 1 (bases 1 to 266)
 AUTHORS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
 , P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
 Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
 Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
 , Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata
 , Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
 , Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomioka, N., Toya
 , T., Tsunoda, Y., Watanabe, A., Watanabe, S., Yamamura, T., Yamana, I.,
 , Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
 , M., Muramatsu, M., and Hayashizaki, Y.
 RIKEN Mouse ESTs (Konno, H., et al.)
 TITLE Unpublished
 JOURNAL Contact: Yoshihide Hayashizaki
 LABORATORY for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
 , N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Thermostabilization and thermocyclization of thermostable enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
 , Y., and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.


```

source
1. .355
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BT1-aqp-f-05-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-BT1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The library
UI-R-BT1 is a subtracted library derived from a mixture of
the following tissues: hippocampus, thalamus, mid-brain,
medulla, corpus striatum, cerebral cortex and testis. For
a detailed description of the library from which this
clone was derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Donald, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_SEQ=None found"
BASE COUNT      30 a      126 c      161 g      37 t      1 others
ORIGIN

Query Match      91.6%; Score 17.4; DB 10; Length 355;
Best Local Similarity 94.7%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGTCTGCAGCGGATGCT 19
      |||||
Db      223 GGGTCTGCAGCGGATGAT 241

RESULT 11
LOCUS      AA892154      386 bp      mRNA      linear      EST 25-JAN-1999
DEFINITION      EST195957 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
                RKIAN02 3' end, mRNA sequence.
ACCESSION      AA892154
VERSION      AA892154.1 GI:3019033
KEYWORDS
SOURCE
ORGANISM      Rattus sp.
                Rattus sp.
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                Rattus.
REFERENCE      1 (bases 1 to 386)
                Lee,N.H., Glodok,A., Chandra,I., Mason,T.M., Quackenbush,J.,
                Kerlavage,A.R. and Adams,M.D.
                Rat Genome Project: Generation of a Rat EST (REEST) Catalog & Rat
                Gene Index
                Unpublished
JOURNAL
COMMENT      Contact: Lee, NH
                The Institute for Genomic Research
                9712, Medical Center Drive, Rockville, MD 20850, USA
                Tel: (301)-838-3529
                Fax: (301)-838-0208
                Email: nhlee@igr.org
                Seq primer: M13-21.
FEATURES
source
1. .386
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="ATCC (ihost):2017749"
/db_xref="taxon:10118"
/clone="RKIAN02"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT      101 a      110 c      96 g      79 t
ORIGIN

Query Match      91.6%; Score 17.4; DB 9; Length 386;
Best Local Similarity 94.7%; Pred. No. 1.8e+03;

```

```

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGTCTGCAGCGGATGCT 19
      |||||
Db      275 GGGTCTGCAGCAGATGCT 293

RESULT 12
CB735745/c
LOCUS      CB735745      463 bp      mRNA      linear      EST 11-APR-2003
DEFINITION      AMGNNUC:NRHY4-00032-B2-A W Rat hypothalamus (10464) Rattus
                norvegicus cDNA clone nrhy4-00032-b2 5', mRNA sequence.
ACCESSION      CB735745
VERSION      CB735745.1 GI:29802948
KEYWORDS
SOURCE
ORGANISM      Rattus norvegicus (Norway rat)
                Rattus norvegicus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                Rattus.
REFERENCE      1 (bases 1 to 463)
                Amgen EST Program.
                Amgen Rat EST Program
                Unpublished
JOURNAL
COMMENT      Contact: Dan Fitzpatrick
                Amgen, Inc
                One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
                Tel: 805 447-4881
                Plate: 00032 row: b column: 2.
FEATURES
source
1. .463
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrhy4-00032-b2"
/clone_lib="W Rat hypothalamus (10464)"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; W Rat
hypothalamus adult female Wistar rat avg. insert size 2.3
kb fraction 6 and 7"
BASE COUNT      77 a      119 c      103 g      103 t      61 others
ORIGIN

Query Match      91.6%; Score 17.4; DB 14; Length 463;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGTCTGCAGCGGATGCT 19
      |||||
Db      259 GGGTCTGCAGCAGATGCT 241

RESULT 13
CB614996/c
LOCUS      CB614996      573 bp      mRNA      linear      EST 07-APR-2003
DEFINITION      AMGNNUC:NRDGL-00012-A1-A nrdgl (10855) Rattus norvegicus cDNA clone
                nrdgl-00012-a1 5', mRNA sequence.
ACCESSION      CB614996
VERSION      CB614996.1 GI:29574884
KEYWORDS
SOURCE
ORGANISM      Rattus norvegicus (Norway rat)
                Rattus norvegicus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                Rattus.
REFERENCE      1 (bases 1 to 573)
                Amgen EST Program.
                Amgen Rat EST Program
                Unpublished
JOURNAL
COMMENT      Contact: Dan Fitzpatrick
                Amgen, Inc
                One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
                Tel: 805 447-4881
                Plate: 00012 row: a column: 1.

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QY 1 GGGTCTGACGGGATGTT 19
 |||
 DB 327 GGGTCTGACGGGATGTT 309

RESULT 16
 BQ059970/c 1164 bp mRNA linear EST 29-MAR-2002
 LOCUS AGENCOURT_6793942 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5816129
 DEFINITION 5', mRNA sequence.
 ACCESSION BQ059970
 VERSION BQ059970.1 GI:19819310
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1164)
 NIH-MGC http://mhc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM2072 row: h column: 18
 High quality sequence start: 19
 High quality sequence stop: 418.
 Location/Qualifiers
 1. 1164
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5816129"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_99"
 /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

BASE COUNT 267 a 268 c 307 g 155 t 167 others
 ORIGIN

Query Match 91.6%; Score 17.4; DB 12; Length 1164;
 Best Local Similarity 94.7%; Pred. No. 2.1e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGACGGGATGTT 19
 |||
 DB 1115 GGGTCTGACGGGATGTT 1097

RESULT 17
 BE887786/c 1562 bp mRNA linear EST 20-OCT-2000
 LOCUS 601511359F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912590 5',
 DEFINITION mRNA sequence.
 ACCESSION BE887786
 VERSION BE887786.1 GI:10343430
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1562)
 NIH-MGC http://mhc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM9731 row: f column: 15
 High quality sequence stop: 6.
 Location/Qualifiers
 1. 1562
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3912590"
 /tissue_type="leiomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_71"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.1 kb."

BASE COUNT 567 a 579 c 208 g 208 t
 ORIGIN

Query Match 91.6%; Score 17.4; DB 10; Length 1562;
 Best Local Similarity 94.7%; Pred. No. 2.2e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGACGGGATGTT 19
 |||
 DB 1152 GGGTCTGACGGGATGTT 1134

RESULT 18
 AK031524 3874 bp mRNA linear HTC 05-DEC-2002
 LOCUS Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
 DEFINITION enriched library, clone:6030447F10 product:hypothetical protein,
 full insert sequence.
 AK031524
 ACCESSION AK031524.1 GI:26327378
 VERSION AK031524.1
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 JOURNAL MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 JOURNAL MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, U., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

TITLE
JOURNAL MEDLINE PUBMED
REFERENCE AUTHORS
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,K., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barah,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaudo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombærts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seta,T., Shibata,Y., Storch,K.F., Suzuki,H., Tono-Oka,K., Wang,K.H., Weltz,C., Whitaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohsaki,S. and Hayashizaki,Y.
TITLE
JOURNAL MEDLINE PUBMED
REFERENCE AUTHORS
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851
5
The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3874)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE
JOURNAL
Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
FEATURES
Source
1. .3874
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"

/db_xref="PANTOM,DB:6030447F10"
/db_xref="taxon:10090"
/clone="6030447F10"
/sex="male"
/tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
42. .815
/note="unnamed protein product; hypothetical protein (evidence: Procrest,NCBI CDS Predictor,longest-ORF) putative"
/codon_start=1
/protein_id="BAC27433.1"
/db_xref="GI:26327379"
/translation="MEEGSAAPPLNMDYLERCFARRVCISFGLWICACCMIAAH TLILYLCCTKCSQDQSTLCAAFCLTSLCDTVGAILRQLTIQFTGAYLAVDPMN FMPTLFPVCGSKSKSKSGQSSRRRRRHURASVPALPLSLGPMATPAKAPAP VRGPORRLGSLQENPEVFGLGAIAGFSWASRIPEFSNIVRLGWGWGRASRGI RSRWRMDVPVWGTHVFLRSQYMTAVRGVCAWCVCMCE"
BASE COUNT 887 a 1033 c 1053 g 901 t
ORIGIN
Query Match 91.6%; Score 17.4; DB 11; Length 3874;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGTCTGCAGCGGATGCT 19
Db 1784 GGGCTTGACGGGATGCT 1802
RESULT 19
BZ554088/c 993 bp DNA linear GSS 17-DEC-2002
LOCUS
DEFINITION
BZ554088 pacs1-60_4515.x1 pacs1-60 Pseudomonas aeruginosa genomic clone
ACCESSION
BZ554088
VERSION
BZ554088.1 GI:27161002
KEYWORDS
GSS.
SOURCE
Pseudomonas aeruginosa
ORGANISM
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
REFERENCE
1 (bases 1 to 993)
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M., Burns,J.L., Kaul,R. and Olsen,M.V.
Whole-Genome-Sequence variation among multiple isolates of Pseudomonas aeruginosa library
J. Bacteriol., (2002) In press
COMMENT
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
FEATURES
Source
1. .993
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="1-60"
/db_xref="taxon:287"
/clone="pacs1-60_4515"
/clone_lib="pacs1-60"
/note="clinical isolate 1-60 whole genomic shotgun library."
BASE COUNT 165 a 298 c 293 g 236 t 1 others
ORIGIN
Query Match 89.5%; Score 17; DB 29; Length 993;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGTCTGACGGGATGG 18
 |||||
 Db 366 GGTCTGACGGGATGG 350

RESULT 20
 BJ239259 206 bp mRNA linear EST 17-SEP-2002
 LOCUS BJ239259 Y. Ogihara unpublished cDNA library, wh_e Triticum
 DEFINITION aestivum cDNA clone whes106 3', mRNA sequence.
 ACCESSION BJ239259
 VERSION BJ239259.1 GI:23082419
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Triticum.
 1 (bases 1 to 206)
 Ogihara, Y. and Murai, K.
 Expressed genes in Triticum aestivum
 Unpublished
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 1. 206
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="whes106"
 /tissue_type="seed DPA10"
 /dev_stage="Peekes' scale 11.2"
 /clone_lib="Y. Ogihara unpublished cDNA library, wh_e"

BASE COUNT 35 a 46 c 79 g 44 t 2 others

ORIGIN

Query Match 86.3%; Score 16.4; DB 12; Length 206;
 Best Local Similarity 94.4%; Pred. No. 4.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTCTGACGGGATGGT 19
 |||||
 Db 89 GGTCTGACGGGATGGT 106

RESULT 21
 AM612888 214 bp mRNA linear EST 23-MAR-2000
 LOCUS hh37g01.x1 NCI_CGAP_Col4 Homo sapiens cDNA clone IMAGE:2957328 3',
 DEFINITION mRNA sequence.
 ACCESSION AM612888
 VERSION AM612888.1 GI:7318074
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 214)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.

JOURNAL
 AUTHORS
 TITLE
 COMMENT

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 image.llnl.gov/image/html/iresources.shtml
 Seq primer: -40UP from Gibco.

FEATURES
 source
 1. 214
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2957328"
 /tissue_type="moderately-differentiated adenocarcinoma"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Col4"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"

BASE COUNT 47 a 58 c 71 g 37 t 1 others

ORIGIN

Query Match 86.3%; Score 16.4; DB 9; Length 214;
 Best Local Similarity 94.4%; Pred. No. 4.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCTGACGGGATGG 18
 |||||
 Db 184 GGTCTGACGGGATGG 201

RESULT 22
 AJ460522 240 bp mRNA linear EST 24-MAY-2002
 LOCUS AJ460522 S00002 Hordeum vulgare subsp. vulgare cDNA clone
 DEFINITION S0000200067D02F1, mRNA sequence.
 ACCESSION AJ460522
 VERSION AJ460522.1 GI:21059442
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 1 (bases 1 to 240)
 Saren, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.
 Barley EST's
 Unpublished
 Contact: Schulman AH
 Institute of Biotechnology
 University of Helsinki
 P.O.Box 56 (Vikinkaari 6A), University of Helsinki FIN-00014,
 Finland.
 Location/Qualifiers
 1. 240
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Saana"
 /db_xref="taxon:112509"
 /clone="S0000200067D02F1"
 /dev_stage="Embryo"
 /clone_lib="S00002"
 /note="1 day after pollination"

BASE COUNT 47 a 87 c 65 g 41 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 9; Length 240;
 Best Local Similarity 94.4%; Pred. No. 4.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTCTGACGGGATGGT 19
 |||||

Db 192 GGTCTGAGCGGATGCT 175

RESULT 23
LOCUS BJ293359/c
DEFINITION BJ293359 Y. Ogihara unpublished cDNA library, wh_SL Triticum
ACCESSION BJ293359
VERSION BJ293359
KEYWORDS BJ293359.1 GI:23150883
SOURCE EST.
ORGANISM Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 253)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
Source
1..253
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whsl31117"
/tissue_type="seed DPA30"
/dev_stage="Fekkes" scale 11.3"
/clone_lib="Y. Ogihara unpublished cDNA library, wh_SL"
48 a 90 c 74 g 41 t

BASE COUNT
ORIGIN

Query Match 86.3%; Score 16.4; DB 12; Length 253;
Best Local Similarity 94.4%; Pred. No. 4.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTCTGACGGGATGCT 19
|||||

Db 207 GGTCTGAGCGGATGCT 190

RESULT 24
LOCUS BJ299950
DEFINITION BJ299950 Y. Ogihara unpublished cDNA library, wh_SL Triticum
ACCESSION BJ299950
VERSION BJ299950
KEYWORDS BJ299950.1 GI:23154630
SOURCE EST.
ORGANISM Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 284)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
Source
Location/Qualifiers
1..284
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whsl32119"
/tissue_type="seed DPA30"
/dev_stage="Fekkes" scale 11.3"
/clone_lib="Y. Ogihara unpublished cDNA library, wh_SL"
53 a 67 c 101 g 59 t 4 others

BASE COUNT
ORIGIN

Query Match 86.3%; Score 16.4; DB 12; Length 284;
Best Local Similarity 94.4%; Pred. No. 4.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTCTGACGGGATGCT 19
|||||

Db 34 GGTCTGAGCGGATGCT 51

RESULT 25
LOCUS BJ299963
DEFINITION BJ299963 Y. Ogihara unpublished cDNA library, wh_SL Triticum
ACCESSION BJ299963
VERSION BJ299963
KEYWORDS BJ299963.1 GI:23154638
SOURCE EST.
ORGANISM Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 292)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
Source
Location/Qualifiers
1..292
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whsl32n06"
/tissue_type="seed DPA30"
/dev_stage="Fekkes" scale 11.3"
/clone_lib="Y. Ogihara unpublished cDNA library, wh_SL"
45 a 82 c 105 g 58 t 2 others

BASE COUNT
ORIGIN

Query Match 86.3%; Score 16.4; DB 12; Length 292;
Best Local Similarity 94.4%; Pred. No. 4.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTCTGACGGGATGCT 19
|||||

Db 34 GGTCTGAGCGGATGCT 51

RESULT 26
LOCUS CA644225
DEFINITION CA644225 292 bp mRNA linear EST 23-NOV-2002
wreln.pk0078.h1 wreln Triticum aestivum cDNA clone wreln.pk0078.h1
5' end, mRNA sequence.

ACCESSION CA644225
 VERSION GI:25222521
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Triticum.
 1 (bases 1 to 292)
 Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
 Miao, G., Caraher, N. and Hanafey, M.K.
 Dupont wheat cDNA Sequence
 Unpublished
 COMMENT Contact: Scott V. Tingey
 Crop Genetics
 B. I. Dupont de Nemours and Company
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2602
 Fax: 302-631-2607
 Email: Scott.V.Tingey@USA.dupont.com
 Seq primer: M13.
 Location/Qualifiers
 1..292
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone="wreln.pk0078.h1"
 /tissue_type="root"
 /clone_lib="wreln"
 /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
 XhoI; Wheat (Triticum aestivum L.) root; normalized from
 wreln library"
 BASE COUNT 58 a 67 c 103 g 62 t 2 others
 ORIGIN
 Query Match 86.3%; Score 16.4; DB 14; Length 292;
 Best Local Similarity 94.4%; Pred. No. 4.7e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GGCTGCAGCGGATGT 19
 |||||
 Db 177 GGCTGCAGCGGATGT 194
 RESULT 27
 BI013302 324 bp mRNA linear EST 13-JUN-2001
 LOCUS PM4-ET0154-210101-010-d07 ET0154 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BI013302
 VERSION BI013302.1 GI:14417373
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 324)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 , M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922

Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&tl2=PM4-ET0154-
 210101-010-d07&tl3=2001-01-21&tl4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 13
 High quality sequence stop: 324.
 Location/Qualifiers
 1..324
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="ET0154"
 /note="Organ: lung tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 54 a 83 c 112 g 75 t
 ORIGIN
 Query Match 86.3%; Score 16.4; DB 12; Length 324;
 Best Local Similarity 94.4%; Pred. No. 4.8e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGCTGCAGCGGATGG 18
 |||||
 Db 257 GGCTGCAGCAGATGG 274
 RESULT 28
 BU974641/c 336 bp mRNA linear EST 22-OCT-2002
 LOCUS HB28J24r BC Hordeum vulgare subsp. vulgare cDNA clone HB28J24
 DEFINITION 5-PRIME, mRNA sequence.
 ACCESSION BU974641
 VERSION BU974641.1 GI:24225434
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 1 (bases 1 to 336)
 Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
 TITLE Barley ESTs from developing seeds
 JOURNAL Unpublished
 COMMENT Contact: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert Length: 336 Std Error: 0.00
 Plate: 28 row: J column: 24
 Seq primer: M13rev.
 Location/Qualifiers
 1..336
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Darke"
 /db_xref="GABI:239491"
 /db_xref="taxon:112509"
 /clone="HB28J24"
 /tissue_type="developing caryopsis"
 /dev_stage="8-15 DAP (days after pollination)"
 /lab_host="XU10-Gold"

```

/clone_lib="BC"
/Note="Vector: pBluescript SK+, Site_1: EcoRI (5'-end of
CDNA); Site_2: XhoI (3'-end of cDNA); developing caryopsis
, 8-15 DAP(days after pollination) Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable."
BASE COUNT      67 a      122 c      91 g      56 t
ORIGIN

Query Match      86.3%; Score 16.4; DB 13; Length 336;
Best Local Similarity 94.4%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGTCTGCAGCGGATGCT 19
      ||||| ||||| |||||
Db      212 GGTCTGCAGCGGATGCT 195

RESULT 29
R25769      350 bp      mRNA      linear      EST 24-APR-1995
LOCUS      yh43f06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone
DEFINITION      IMAGE:132515 5', mRNA sequence.
ACCESSION      R25769
VERSION      R25769.1 GI:781904
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 350)
AUTHORS      Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaekis, E., Waterston
, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE      The WashU-Merck EST Project
JOURNAL      Unpublished
COMMENT      Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 484
High quality sequence stops: 220
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 484 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 220.
Location/Qualifiers
1..350
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:538127"
/db_xref="taxon:9606"
/clone="IMAGE:132515"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta Nb2HP"
/Note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AACTGAGAAATTGGCGGCCGAGAAATTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library

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went through one round of normalization. Library
constructed by Bento Soares and M.Patima Bernaldo. "
BASE COUNT      81 a      107 c      104 g      53 t
ORIGIN

Query Match      86.3%; Score 16.4; DB 14; Length 350;
Best Local Similarity 94.4%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTCTGCAGCGGATGG 18
      ||||| ||||| |||||
Db      89 GGTCTGCAGCAGATGG 72

RESULT 30
AW769047      355 bp      mRNA      linear      EST 04-MAY-2000
LOCUS      h157h11.x1 NCI CGAP Col4 Homo sapiens cDNA clone IMAGE:3005349 3'
DEFINITION      similar to TR:Q60997 Q60997 CRP-DUCTIN PRECURSOR ;, mRNA sequence.
ACCESSION      AW769047
VERSION      AW769047.1 GI:7701073
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 355)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL, send email to:
info@image.lnl.gov
Possible reversed clone: polyT not found
Seq primer: -40UP from Gdbco
High quality sequence stop: 225.
Location/Qualifiers
1..355
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3005349"
/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Col4"
/Note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"
BASE COUNT      80 a      101 c      111 g      63 t
ORIGIN

Query Match      86.3%; Score 16.4; DB 9; Length 355;
Best Local Similarity 94.4%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTCTGCAGCGGATGG 18
      ||||| ||||| |||||
Db      184 GGTCTGCAGCTGATGG 201

RESULT 31
AI473980      362 bp      mRNA      linear      EST 09-MAR-1999
LOCUS      tm04g09.x1 NCI CGAP Col4 Homo sapiens cDNA clone IMAGE:2155648 3'
DEFINITION

```

similar to TR:Q60997 Q60997 CRP-DUCTIN PRECURSOR ;, mRNA sequence.

ACCESSION AI473980
VERSION AI473980.1 GI:4327025
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 362)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.lnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 197.
Location/Qualifiers

FEATURES
source
1..362
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2155648"
/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Col4"
/note="Organ: colon; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"

BASE COUNT 84 a 105 c 105 g 64 t 4 others
ORIGIN

Query Match 86.3%; Score 16.4; DB 9; Length 362;
Best Local Similarity 94.4%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGG 18
|||||
Db 184 GGGTCTGCAGCTGATGG 201

RESULT 32
LOCUS BF112016 369 bp mRNA linear EST 20-OCT-2000
DEFINITION 7137f04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523711 3', mRNA sequence.
ACCESSION BF112016
VERSION BF112016.1 GI:10941629
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 369)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers

FEATURES

source
1..369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3523711"
/lab_host="DH10B"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares Nb2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 59 a 96 c 123 g 91 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 10; Length 369;
Best Local Similarity 94.4%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGG 18
|||||
Db 313 GGGTCTGCAGCAGGATGG 330

RESULT 33
LOCUS BQ189288/c 380 bp mRNA linear EST 30-APR-2002
DEFINITION UI-E-EJ1-ajv-b-09-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone IMAGE:3523711 3', mRNA sequence.
ACCESSION BQ189288
VERSION BQ189288.1 GI:20364839
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 380)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 REVERSE.
Location/Qualifiers

FEATURES
source
1..380
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

```
/clone="UI-E-EJ1-ajv-b-09-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-EJ1"
/notes="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJ1 is a subcloned cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA
; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT;
optic nerve, CCATTAGTCG; retina, CCGCG; Retina Foveal and
Macular, GTCC; RPE and Choroid, ACCCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
```

BASE COUNT 97 a 105 c 112 g 66 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 13; Length 380;
Best Local Similarity 94.4%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 GGGTCTGCAGCGGATCG 18
|||||
Db 304 GGGTCTGCAGCAGATCG 287

RESULT 34
LOCUS AW662148 382 bp mRNA linear EST 06-APR-2000
DEFINITION hi20b08.x1 NCI CGAP GUI Homo sapiens cDNA clone IMAGE:2972823 3'
similar to TR:Q60997 Q60997 CRP-DUCTIN PRECURSOR ;, mRNA sequence.
AW662148
AW662148.1 GI:7454685
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 382)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/resources.shcml
Seq primer: -40UP from Gibco
High quality sequence stop: 233.
Location/Qualifiers
1..382
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2972823"
/tissue_type="2 pooled high-grade transitional cell
tumors"

FEATURES
source

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/lab_host="DH10B"
/clone_lib="NCI_CGAP_GUI"
/notes="Organ: gentourinary tract; Vector: pCMV-SPORT6;
Site_1: SalI; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Library constructed by Life
Technologies."
```

BASE COUNT 88 a 108 c 118 g 68 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 9; Length 382;
Best Local Similarity 94.4%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 GGGTCTGCAGCGGATCG 18
|||||
Db 184 GGGTCTGCAGCTGATCG 201

RESULT 35
LOCUS AA613554 382 bp mRNA linear EST 31-OCT-1997
DEFINITION ng22e02.s1 NCI_CGAP_Col0 Homo sapiens cDNA clone IMAGE:1144634 3',
mRNA sequence.
AA613554
AA613554.1 GI:2464592
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 382)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 496 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
Location/Qualifiers
1..382
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1144634"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Col0"
/notes="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
RER+ colon tumor, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo (N-Soares4)."

BASE COUNT 90 a 98 c 110 g 84 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 9; Length 382;
Best Local Similarity 94.4%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 GGGTCTGCAGCGGATCG 18
|||||

Db 361 GGGTCTGCAGCTGATGG 378

RESULT 36
BE411862/c

LOCUS
DEFINITION BE411862 394 bp mRNA linear EST 26-JUL-2000
ISC010.A09F990908 ITEC ISC Barley leaf Library Hordeum vulgare
subsp. vulgare cDNA clone ISC010.A09, mRNA sequence.

ACCESSION
VERSION BE411862
KEYWORDS
SOURCE BE411862.1 GI:9409636
ORGANISM EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.

REFERENCE
AUTHORS 1 (bases 1 to 394)
Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier
, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,
Herrmann, R.G., Holton, T., Jacquemlin, J.M., Jia, J., Joudrier, P.,
Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y.,
Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,
Sorrells, M., Warburton, M. and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)
Contact: Pecchioni N
Istituto Sperimentale per la Cerealicoltura
via San Protaso 302, I-29017 Fiorenzuola d'Arda (PC), ITALY
Tel: 39 0523 983758
Fax: 39 0523 983750
Email: n.pecchioni@iol.it
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.

TITLE
JOURNAL
COMMENT

FEATURES
source
1.394
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Nure"
/db_xref="taxon:112509"
/clone="ISC010.A09"
/tissue_type="leaf"
/dev_stage="first leaf, cold stress"
/clone_lib="ITEC ISC Barley leaf Library"
/note="Vector: UNI-ZAP XR; 0.7-2.0 Kbp average insert
size."

BASE COUNT 75 a 143 c 105 g 71 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 10; Length 394;
Best Local Similarity 94.4%; Pred. NO. 4.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTCTGCAGCGGATGGT 19
||||| |||||||

Db 241 GGTCTGCAGCGGATGGT 224

RESULT 37
BM443000/c

LOCUS
DEFINITION BM443000 400 bp mRNA linear EST 23-JUL-2002
EBro02_SQ002_C13_R root, 3 week, hydroponic grown, low nitrogen, cv
Optic, EBro02 Hordeum vulgare subsp. vulgare cDNA clone
EBro02_SQ002_C13_5', mRNA sequence.

ACCESSION
VERSION BM443000
KEYWORDS BM443000.2 GI:21947654
SOURCE EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.

REFERENCE
1 (bases 1 to 400)

AUTHORS Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudge, S., Cardie, L.,
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished
On Feb 1, 2002 this sequence version replaced gi:18473763.

TITLE
JOURNAL
COMMENT

CONTACT: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.

FEATURES
source
1.400
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Optic"
/db_xref="taxon:112509"
/clone="EBro02_SQ002_C13"
/tissue_type="root"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="root, 3 week, hydroponic grown, low nitrogen,
cv Optic, EBro02"
/note="Vector: pSPORT1, Site 1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from roots of 3 week old Nitrogen stressed barley
plants. Developed as part of the barley transcriptome
resources of BBSRC/SEERAD funded cereal IGF (Investigating
Gene Function) project."

BASE COUNT 77 a 148 c 104 g 71 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 12; Length 400;
Best Local Similarity 94.4%; Pred. NO. 4.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTCTGCAGCGGATGGT 19
||||| |||||||

Db 254 GGTCTGCAGCGGATGGT 237

RESULT 38
CB871117

LOCUS
DEFINITION CB871117 402 bp mRNA linear EST 23-APR-2003
HC02F21Y HC Hordeum vulgare subsp. vulgare cDNA clone HC02F21
3-PRIME, mRNA sequence.

ACCESSION
VERSION CB871117
KEYWORDS CB871117.1 GI:30073097
SOURCE EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.

REFERENCE
1 (bases 1 to 402)
Varshney, R.K., Zhang, H., Burton, R., Stein, N., Langridge, P. and
Graner, A.
Barley ESTs from coleoptile tissue
Unpublished
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 402 Std Error: 0.00
Plate: 2 row: F column: 21
Seq primer: SP6.

TITLE
JOURNAL
COMMENT

FEATURES
Location/Qualifiers


```
source
1..402
/mol_type="mRNA"
/strain="cv tokak"
/db_xref="GABI:549519"
/db_xref="taxon:112509"
/clone="HC02F21"
/tissue_type="Root"
/dev_stage="3 week old"
/clone_1b="HC"
/note="6 and 10 hour drought stress by placing plants on
moist paper (75% rel. humidity) in light"

BASE COUNT      75 a      106 c      140 g      81 t
ORIGIN

Query Match      86.3%; Score 16.4; DB 14; Length 402;
Best Local Similarity 94.4%; Pred. No. 4.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGTCTGACGGGATGGT 19
        |||||
Db      186 GGTCTGACGGGATGGT 203

RESULT 39
BH306574/c      403 bp      DNA      linear      GSS 30-NOV-2001
LOCUS
DEFINITION      CH230-192M6.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-192M6, genomic survey sequence.
BH306574
BH306574.1      GI:17218982
GSS.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 403)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). BAC end
page: http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html
Plate: 192 row: M column: 6
Seq primer: T7
Class: BAC ends.

FEATURES
source
1..403
/location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-192M6"
/sex="Female"
/cell_type="Brain"
/clone_1b="CHORI-230 Segment 1"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"

BASE COUNT      106 a      108 c      77 g      112 t
```

```
ORIGIN
Query Match      86.3%; Score 16.4; DB 28; Length 403;
Best Local Similarity 94.4%; Pred. No. 4.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGTCTGACGGGATGG 18
        |||||
Db      265 GGGTCTGACGAGGATGG 248

RESULT 40
AI492104      406 bp      mRNA      linear      EST 30-MAR-1999
LOCUS
DEFINITION      tg07b01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108041 3',
mRNA sequence.
AI492104
AI492104.1      GI:4393107
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 498 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES
source
1..406
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2108041"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/clone_1b="NCI CGAP CLL1"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT      94 a      107 c      115 g      90 t
ORIGIN

Query Match      86.3%; Score 16.4; DB 9; Length 406;
Best Local Similarity 94.4%; Pred. No. 4.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGTCTGACGGGATGG 18
        |||||
Db      361 GGGTCTGACGATGG 378

Search completed: January 13, 2004, 16:33:19
Job time : 1197.5 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2004, 17:32:17 ; Search time 126.5 Seconds
(without alignments)
521.578 Million cell updates/sec

Title: US-09-719-737-9

Perfect score: 19

Sequence: 1 gggctcgcagcgsgatggt 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2276164 seqs, 1736306516 residues

Total number of hits satisfying chosen parameters: 4552328

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19	100.0	2694	12	US-10-085-117-12
C 2	19	100.0	2996	12	US-10-085-117-11
C 3	19	100.0	3439	14	US-10-044-090-546
C 4	19	100.0	36595	12	US-10-085-117-10
C 5	16.4	86.3	390	11	US-09-918-995-7315
C 6	16.4	86.3	1194	13	US-10-183-708-49
C 7	16.4	86.3	1194	13	US-09-932-227-49
C 8	16.4	86.3	1824	10	US-09-738-626-109
C 9	16.4	86.3	3309400	10	US-09-738-626-1
C 10	15.8	83.2	153	13	US-10-029-386-14644
C 11	15.8	83.2	504	13	US-10-027-632-6525
C 12	15.8	83.2	504	14	US-10-027-632-6525
C 13	15.8	83.2	507	13	US-10-027-632-188580
C 14	15.8	83.2	507	13	US-10-027-632-188581
C 15	15.8	83.2	507	13	US-10-027-632-188582

16	15.8	83.2	507	13	US-10-027-632-188583	Sequence 188583,
17	15.8	83.2	507	14	US-10-027-632-188580	Sequence 188580,
18	15.8	83.2	507	14	US-10-027-632-188581	Sequence 188581,
19	15.8	83.2	507	14	US-10-027-632-188582	Sequence 188582,
20	15.8	83.2	507	14	US-10-027-632-188583	Sequence 188583,
21	15.8	83.2	589	13	US-10-029-386-941	Sequence 941, App
C 22	15.8	83.2	868	13	US-10-027-632-159729	Sequence 159729,
C 23	15.8	83.2	868	13	US-10-027-632-159729	Sequence 159729,
C 24	15.8	83.2	2940917	13	US-10-027-632-174763	Sequence 174763,
C 25	15.8	83.2	2940917	14	US-10-027-632-174763	Sequence 174763,
C 26	15.4	81.1	1560	12	US-10-369-493-44678	Sequence 44678, A
C 27	15.4	81.1	536165	11	US-09-939-964-1	Sequence 1, Appl1
C 28	15	78.9	121	11	US-09-818-875-1345	Sequence 1345, Ap
C 29	15	78.9	121	11	US-09-818-875-1346	Sequence 1346, Ap
C 30	15	78.9	121	13	US-10-209-787-1345	Sequence 1345, Ap
C 31	15	78.9	121	13	US-10-209-787-1346	Sequence 1346, Ap
C 32	15	78.9	340	12	US-10-429-802-28	Sequence 28, Appl
C 33	15	78.9	401	9	US-09-016-8698-22	Sequence 22, Appl
C 34	15	78.9	404	9	US-09-016-8698-21	Sequence 21, Appl
C 35	15	78.9	1146	13	US-09-908-671-1	Sequence 1, Appl1
C 36	15	78.9	3621	11	US-09-984-664-15	Sequence 15, Appl
C 37	14.8	77.9	52	11	US-09-993-525-11	Sequence 11, Appl
C 38	14.8	77.9	219	15	US-10-156-761-7227	Sequence 7227, Ap
C 39	14.8	77.9	228	13	US-10-339-604-69	Sequence 69, Appl
C 40	14.8	77.9	276	10	US-09-878-574-12285	Sequence 12285, A
C 41	14.8	77.9	312	9	US-09-815-242-7546	Sequence 7546, Ap
C 42	14.8	77.9	312	9	US-09-815-242-9877	Sequence 9877, Ap
C 43	14.8	77.9	319	13	US-10-339-604-35	Sequence 35, Appl
C 44	14.8	77.9	324	13	US-10-339-604-36	Sequence 36, Appl
C 45	14.8	77.9	362	10	US-09-983-965-731	Sequence 731, App

ALIGNMENTS

RESULT 1

US-10-085-117-12/c

; Sequence 12, Application US/10085117

; Publication No. US20030232334A1

; GENERAL INFORMATION:

; APPLICANT: Morris, David W.

; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

; FILE REFERENCE: 529452000121

; CURRENT APPLICATION NUMBER: US/10/085,117

; CURRENT FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: US 09/798,586

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 361

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 2694

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-085-117-12

Query Match

Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19

|||||

Db 97 GGGTCTGCAGCGGATGCT 79

RESULT 2

US-10-085-117-11/c

; Sequence 11, Application US/10085117

; Publication No. US20030232334A1

; GENERAL INFORMATION:

; APPLICANT: Morris, David W.

; APPLICANT: Engelhard, Eric K.

; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

FILE REFERENCE: 529452000121
CURRENT APPLICATION NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2996
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-117-11

Query Match 100.0%; Score 19; DB 12; Length 2996;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
|||||
DB 125 GGGTCTGCAGCGGATGCT 107

RESULT 3
US-10-044-090-546/c

Sequence 546, Application US/10044090
Publication No. US20020137081A1
GENERAL INFORMATION:

APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 546
LENGTH: 3439
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 3420843CB1
US-10-044-090-546

Query Match 100.0%; Score 19; DB 14; Length 3439;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
|||||
DB 273 GGGTCTGCAGCGGATGCT 255

RESULT 4
US-10-085-117-10/c

Sequence 10, Application US/10085117
Publication No. US20030232334A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: 529452000121
CURRENT APPLICATION NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 36595
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-117-10

Query Match 100.0%; Score 19; DB 12; Length 36595;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
|||||
DB 11085 GGGTCTGCAGCGGATGCT 11067

RESULT 5
US-09-918-995-7315/c

Sequence 7315, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7315
LENGTH: 390
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) .. (390)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-7315

Query Match 86.3%; Score 16.4; DB 11; Length 390;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 18
|||||
DB 118 GGGTCTGCAGCTGATGG 101

RESULT 6
US-10-183-708-49/c

Sequence 49, Application US/10183708
Publication No. US20030143679A1
GENERAL INFORMATION:
APPLICANT: VOSSHALL, LESLIE
APPLICANT: AMREIN, HUBERT
APPLICANT: AXEL, RICHARD
TITLE OF INVENTION: GENES ENCODING INSECT ODORANT RECEPTORS AND USES THEREOF
FILE REFERENCE: 0575/58715-AA-PCT-US/JPM/ADM/BUA
CURRENT APPLICATION NUMBER: US/10/183,708
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 09/932,227
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: PCT/US00/04995
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 09/257,706
PRIOR FILING DATE: 1999-02-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn version 3.0
SEQ ID NO 49
LENGTH: 1194
TYPE: DNA
ORGANISM: Drosophila melanogaster DOR119
US-10-183-708-49

Query Match 86.3%; Score 16.4; DB 13; Length 1194;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGTCCTGCAGCGGATGCT 19
 |||||
 Db 933 GGTCCTGCAGCAGGATGCT 916

RESULT 7

```

US-09-932-227-49/c
; Sequence 49, Application US/09932227
; Publication No. US20030186359A1
; GENERAL INFORMATION:
; APPLICANT: VOSSHALL, LESLIE
; APPLICANT: AMREIN, HUBERT
; APPLICANT: AXEL, RICHARD
; TITLE OF INVENTION: GENES ENCODING INSECT ODORANT RECEPTORS AND USES THEREOF
; FILE REFERENCE: 0575/58715-A-PCT-US/JPW/ADM/BJA
; CURRENT APPLICATION NUMBER: US/09/932,227
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/04995
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-932-227-49
DOR119

```

Query Match	86.3%;	Score 16.4;	DB 13;	Length 1194;
Best Local Similarity	94.4%;	Pred. No. 1.2e+02;		
Matches 17; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	2	GGTCTGCAGCGGATGT	19
Db	933	GGTCTGCAGCAGATGT	916

RESULT 8

```

US-09-738-626-109
; Sequence 109, Application US/09738626
; Publication No. US20020197605A1
;
; GENERAL INFORMATION:
;
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
;
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 109
;
; LENGTH: 1824
;
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-109

```

Query Match	86.3%;	Score 16.4;	DB 10;	Length 1824;
Best Local Similarity	94.4%;	Pred. No. 1.2e+02;		
Matches 17; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 2 GGTCTGACGGGATGT 19
|||
Db 301 GGTCCTGACGGGAAGT 318

RESULT 9

```

US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

```

Query Match	86.3%	Score 16.4;	DB 10;	Length 3309400;
Best Local Similarity	94.4%;	Pred. NO. 43;		
Matches 17; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 2 GGTCTGCAGCGGGATGTT 19
103135 GGTCTGCAGCGGGAGGT 103118
Db

RESULT 10

```

US-10-029-386-14644
; Sequence 14644, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENOTYPING
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO. 14644
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR22.166.0
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
; OTHER INFORMATION: SWISSPROT HIT: P32927, EVALUATE 2.00e-16

```

OTHER INFORMATION: NT HIT: g11418060, EVALUE 6.00e-50
OTHER INFORMATION: EST_HUMAN HIT: BF884753.1, EVALUE 1.00e-27
US-10-029-386-14644

Query Match 83.2%; Score 15.8; DB 13; Length 153;
Best Local Similarity 89.5%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
|||||
DB 133 GGGTCTGCAGCAGCGGT 151

RESULT 11

US-10-027-632-6525/c
Sequence 6525, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6525
LENGTH: 504
TYPE: DNA
ORGANISM: Human
US-10-027-632-6525

Query Match 83.2%; Score 15.8; DB 13; Length 504;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
|||||
DB 493 GGGTCTGCAGCAGCGGT 475

RESULT 12

US-10-027-632-6525/c
Sequence 6525, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6525
LENGTH: 504
TYPE: DNA
ORGANISM: Human
US-10-027-632-6525

Query Match 83.2%; Score 15.8; DB 14; Length 504;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
|||||
DB 493 GGGTCTGCAGCAGCGGT 475

RESULT 13

US-10-027-632-188580
Sequence 188580, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 188580
LENGTH: 507
TYPE: DNA
ORGANISM: Human
US-10-027-632-188580

Query Match 83.2%; Score 15.8; DB 13; Length 507;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
|||||
DB 18 GGGTCTGCAGCAGCGGT 36

RESULT 14

US-10-027-632-188581
Sequence 188581, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome

```
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188581
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-188581
```

```
Query Match      83.2%; Score 15.8; DB 13; Length 507;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      1 GGGTCTGCAGCGGATGCT 19
        ||||||||| |||||
Db      18 GGGTCTGCAGCAGGTGCT 36
```

```
RESULT 15
US-10-027-632-188582
; Sequence 188582, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188582
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-188582
```

```
Query Match      83.2%; Score 15.8; DB 13; Length 507;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      1 GGGTCTGCAGCGGATGCT 19
        ||||||||| |||||
```

```
Db      18 GGGTCTGCAGCAGGTGCT 36
```

```
RESULT 16
US-10-027-632-188583
; Sequence 188583, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188583
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-188583
```

```
Query Match      83.2%; Score 15.8; DB 13; Length 507;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      1 GGGTCTGCAGCGGATGCT 19
        ||||||||| |||||
Db      18 GGGTCTGCAGCAGGTGCT 36
```

```
RESULT 17
US-10-027-632-188580
; Sequence 188580, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188580
; LENGTH: 507
```

TYPE: DNA
ORGANISM: Human
US-10-027-632-188580

Query Match 83.2%; Score 15.8; DB 14; Length 507;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
|||||
Db 18 GGGTCTGCAGCAGGTGCT 36

RESULT 18
US-10-027-632-188581
Sequence 188581, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 188581

LENGTH: 507

TYPE: DNA

ORGANISM: Human

US-10-027-632-188581

Query Match 83.2%; Score 15.8; DB 14; Length 507;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
|||||
Db 18 GGGTCTGCAGCAGGTGCT 36

RESULT 19
US-10-027-632-188582
Sequence 188582, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 188582

QY 1 GGGTCTGCAGCGGATGCT 19
|||||
Db 18 GGGTCTGCAGCAGGTGCT 36

Query Match 83.2%; Score 15.8; DB 14; Length 507;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
|||||
Db 18 GGGTCTGCAGCAGGTGCT 36

RESULT 20
US-10-027-632-188583

Sequence 188583, Application US/10027632

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 188583

LENGTH: 507

TYPE: DNA

ORGANISM: Human

US-10-027-632-188583

Query Match 83.2%; Score 15.8; DB 14; Length 507;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
|||||
Db 18 GGGTCTGCAGCAGGTGCT 36

RESULT 21
US-10-029-386-941

Sequence 941, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE


```
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 941
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR22_166.0
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
; OTHER INFORMATION: NT HIT: g11418060, EVALUE 2.00e-50
; OTHER INFORMATION: EST_HUMAN HIT: BF884753.1, EVALUE 3.00e-28
; OTHER INFORMATION: SWISSPROT HIT: P32927, EVALUE 3.00e-16
US-10-029-386-941
```

```
Query Match      83.2%; Score 15.8; DB 13; Length 589;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 GGGTCTGCAGCGGATGCT 19
         |||||
Db      412 GGGTCTGCAGCAGGACGCT 430
```

```
RESULT 22
US-10-027-632-159729/c
; Sequence 159729, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159729
; LENGTH: 868
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-159729
```

```
Query Match      83.2%; Score 15.8; DB 13; Length 868;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 GGGTCTGCAGCGGATGCT 19
         |||||
Db      372 GGGTCTGCAGGCGGACGCT 354
```

```
RESULT 23
US-10-027-632-159729/c
```

```
; Sequence 159729, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159729
; LENGTH: 868
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-159729
```

```
Query Match      83.2%; Score 15.8; DB 14; Length 868;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 GGGTCTGCAGCGGATGCT 19
         |||||
Db      372 GGGTCTGCAGGCGGACGCT 354
```

```
RESULT 24
US-10-027-632-174763/c
; Sequence 174763, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174763
; LENGTH: 2940917
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(2940917)
```

OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174763

Query Match 83.2%; Score 15.8; DB 13; Length 2940917;
Best Local Similarity 89.5%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
Db 299508 GGGTATTTCAGCGGATGCT 299490

RESULT 25
US-10-027-632-174763/c
Sequence 174763, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 174763

LENGTH: 2940917

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(2940917)

OTHER INFORMATION: n = A,T,C or G

US-10-027-632-174763

Query Match 83.2%; Score 15.8; DB 14; Length 2940917;
Best Local Similarity 89.5%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
Db 299508 GGGTATTTCAGCGGATGCT 299490

RESULT 26
US-10-369-493-44678
Sequence 44678, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 44678
LENGTH: 1560
TYPE: DNA
ORGANISM: SYNECHOCOCCUS SP. WH 8102
US-10-369-493-44678

Query Match 81.1%; Score 15.4; DB 12; Length 1560;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GTCTGCAGCGGATGCT 19
Db 1373 GTCTGCAGCGGATGCT 1389

RESULT 27

US-09-939-964-1/c

Sequence 1, Application US/09939964

Publication No. US20030054522A1

GENERAL INFORMATION:

APPLICANT: Rosenthal, Andre

APPLICANT: Freiberg, Christoph

APPLICANT: Perret, Xavier Philippe

APPLICANT: Broughton, William John

TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic

FILE REFERENCE: CARP0068

CURRENT APPLICATION NUMBER: US/09/939,964

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 09/214,808

PRIOR FILING DATE: 1999-06-22

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 536165

TYPE: DNA

ORGANISM: Rhizobium

US-09-939-964-1

Query Match 81.1%; Score 15.4; DB 11; Length 536165;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GTCTGCAGCGGATGCT 19
Db 457877 GTCTGCAGCGGATGCT 457861

RESULT 28
US-09-818-875-1345
Sequence 1345, Application US/09818875

Publication No. US20030051270A1

GENERAL INFORMATION:

APPLICANT: Kmiec, Eric B.

APPLICANT: Gamper, Howard B.

APPLICANT: Rice, Michael C.

TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single

TITLE OF INVENTION: Stranded Oligonucleotides

FILE REFERENCE: Napro-4

CURRENT APPLICATION NUMBER: US/09/818,875

CURRENT FILING DATE: 2001-03-27

PRIOR APPLICATION NUMBER: US 60/192,176

PRIOR FILING DATE: 2000-03-27

PRIOR APPLICATION NUMBER: US 60/192,179

PRIOR FILING DATE: 2000-03-27

PRIOR APPLICATION NUMBER: US 60/208,538

PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: US 60/244,989

PRIOR FILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 4385

SOFTWARE: Friedman macro Napro4

; SEQ ID NO 1345
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-1345

Query Match
Best Local Similarity 100.0%; Score 15; DB 11; Length 121;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGTCTGCAGCGGGA 15
Db 89 GGGTCTGCAGCGGGA 103

RESULT 29
US-09-818-875-1346/c
; Sequence 1346, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:

; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1346
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-1346

Query Match
Best Local Similarity 100.0%; Score 15; DB 11; Length 121;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGTCTGCAGCGGGA 15
Db 33 GGGTCTGCAGCGGGA 19

RESULT 30
US-10-209-787-1345

; Sequence 1345, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:

; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538

; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1345
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-1345

Query Match
Best Local Similarity 100.0%; Score 15; DB 13; Length 121;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGTCTGCAGCGGGA 15
Db 89 GGGTCTGCAGCGGGA 103

RESULT 31
US-10-209-787-1346/c
; Sequence 1346, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:

; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1346
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-1346

Query Match
Best Local Similarity 100.0%; Score 15; DB 13; Length 121;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGTCTGCAGCGGGA 15
Db 33 GGGTCTGCAGCGGGA 19

RESULT 32
US-10-429-802-28

; Sequence 28, Application US/10429802
; Publication No. US20030228285A1
; GENERAL INFORMATION:

; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: WONG, KA YIN
; APPLICANT: ZOU, YIYU
; TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
; FILE REFERENCE: UTSC:752US
; CURRENT APPLICATION NUMBER: US/10/429,802
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/377,672

PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 340
TYPE: DNA
ORGANISM: Homo sapiens
US-10-429-802-28

Query Match 78.9%; Score 15; DB 12; Length 340;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGA 15
|||||
Db 264 GGGTCTGCAGCGGA 278

RESULT 33

US-09-016-869B-22
Sequence 22, Application US/09016869B
Patent No. US20020082392A1
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
TITLE OF INVENTION: Uses Related Thereto
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ropes & Gray
STREET: One International Place
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016, 869B
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/893,274
FILING DATE: 15-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: GPCI-P10-071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 951-7739
TELEFAX: (617) 951-7050
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-016-869B-22

Query Match 78.9%; Score 15; DB 9; Length 401;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGA 15
|||||
Db 18 GGGTCTGCAGCGGA 32

RESULT 34

US-09-016-869B-21
Sequence 21, Application US/09016869B
Patent No. US20020082392A1
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
TITLE OF INVENTION: Uses Related Thereto
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ropes & Gray
STREET: One International Place
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016, 869B
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/893,274
FILING DATE: 15-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: GPCI-P10-071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 951-7739
TELEFAX: (617) 951-7050
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
US-09-016-869B-21

Query Match 78.9%; Score 15; DB 9; Length 404;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGGA 15
|||||
Db 112 GGGTCTGCAGCGGGA 126

RESULT 35

US-09-908-671-1
; Sequence 1, Application US/09908671
; Publication No. US20030138928A1

GENERAL INFORMATION:
APPLICANT: CARSON, DENNIS A.

NOBORI, TSUTOMU

TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR
DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND CA
TREATMENT

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: California

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/908,671

FILING DATE: 18-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/227,800

FILING DATE: 14-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: HOWELLS, STACY L.

REGISTRATION NUMBER: 34,842

REFERENCE/DOCKET NUMBER: 07340/023001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1146 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:

LIBRARY: 5'region of CDK4I (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1146

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-908-671-1

Query Match 78.9%; Score 15; DB 13; Length 1146;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGGA 15
|||||
Db 525 GGGTCTGCAGCGGGA 539

RESULT 36
US-09-984-664-15

; Sequence 15, Application US/09984664
; Publication No. US2003009950A1

GENERAL INFORMATION:

APPLICANT: Hanna, Michelle

TITLE OF INVENTION: Molecular Detection Systems Utilizing Reiterative Oligonucleotide

FILE REFERENCE: 2072.0010000

CURRENT APPLICATION NUMBER: US/09/984,664

CURRENT FILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.0

SEQ ID NO 15

LENGTH: 3621

TYPE: DNA

ORGANISM: Homo sapiens

US-09-984-664-15

Query Match 78.9%; Score 15; DB 11; Length 3621;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGGA 15
|||||
Db 2378 GGGTCTGCAGCGGGA 2392

RESULT 37

US-09-993-525-11

; Sequence 11, Application US/09993525
; Publication No. US2003003203A1

GENERAL INFORMATION:

APPLICANT: Diaz-Torres, Maria

TITLE OF INVENTION: Production of Secreted Polypeptides

FILE REFERENCE: GC618

CURRENT APPLICATION NUMBER: US/09/993,525

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: WO PCT/US99/31010

PRIOR FILING DATE: 1999-12-21

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11

LENGTH: 52

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: primer

US-09-993-525-11

Query Match 77.9%; Score 14.8; DB 11; Length 52;
Best Local Similarity 88.9%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATCG 18
|||||
Db 3 GCGCCTGCAGCGGATCG 20

RESULT 38

US-10-156-761-7227/C

; Sequence 7227, Application US/10156761
; Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

```

; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7227
; LENGTH: 219
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(219)
US-10-156-761-7227
```

```

Query Match      77.9%; Score 14.8; DB 15; Length 219;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 GGGTCTGCAGCGGATGG 18
          |||||
Db      103 GGGTCGGCAGCGGCTGG 86
```

```

RESULT 39
US-10-339-604-69/c
; Sequence 69, Application US/10339604
; Publication No. US20030152982A1
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRANCOISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: Oligonucleotide Molecules for Use in Detection of Mycobacterium
; TITLE OF INVENTION: Antibiotic Resistance
; FILE REFERENCE: 1657.0010001
; CURRENT APPLICATION NUMBER: US/10/339,604
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US/09/722,319
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/750,088
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: PCT/EP95/02230
; PRIOR FILING DATE: 1995-06-09
; PRIOR APPLICATION NUMBER: EP 94870093.5
; PRIOR FILING DATE: 1994-06-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: n can be any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: n can be any nucleotide
US-10-339-604-69
```

```

Query Match      77.9%; Score 14.8; DB 13; Length 228;
Best Local Similarity 88.9%; Pred. No. 9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 GGGTCTGCAGCGGATGG 18
          |||||
Db      76 GGGTCTGCAGCGGATGG 59
```

```

RESULT 40
US-09-878-574-12285/c
; Sequence 12285, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 12285
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701065580H1
US-09-878-574-12285
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```

Query Match      77.9%; Score 14.8; DB 10; Length 276;
Best Local Similarity 88.9%; Pred. No. 8.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY      1 GGGTCTGCAGCGGATGG 18
          |||||
Db      59 GGGTCTGCATCGGAGG 42
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Search completed: January 13, 2004, 21:03:11
Job time : 139.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: January 13, 2004, 15:53:18 ; Search time 36.5 Seconds
(without alignments)
229.761 Million cell updates/sec

Title: US-09-719-737-9
Perfect score: 19
Sequence: 1 ggggtctgcagcggtatggt 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/1/ina/PCUS_COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	100.0	3475	1	US-07-960-389-1 Sequence 1, Appli
C 2	16.4	86.3	1350	4	US-09-252-991A-4370 Sequence 4370, Ap
C 3	16.4	86.3	1455	4	US-09-252-991A-4216 Sequence 4216, Ap
C 4	16.4	86.3	5802	4	US-09-341-587-4 Sequence 4, Appli
C 5	16.4	86.3	28720	4	US-09-341-587-7 Sequence 7, Appli
C 6	15.4	81.1	480	4	US-09-252-991A-3819 Sequence 3819, Ap
C 7	15.4	81.1	897	4	US-09-252-991A-3775 Sequence 3775, Ap
C 8	15.4	81.1	1272	4	US-09-252-991A-3591 Sequence 3591, Ap
C 9	15.4	81.1	536165	4	US-09-214-808-1 Sequence 1, Appli
C 10	15.4	81.1	4403765	3	US-09-103-840A-2 Sequence 2, Appli
C 11	15.4	81.1	4411529	3	US-09-103-840A-1 Sequence 1, Appli
C 12	15	78.9	401	3	US-08-581-918A-27 Sequence 27, Appli
C 13	15	78.9	401	3	US-08-346-147B-27 Sequence 27, Appli
C 14	15	78.9	401	3	US-08-497-214D-27 Sequence 27, Appli
C 15	15	78.9	404	3	US-08-581-918A-26 Sequence 26, Appli
C 16	15	78.9	404	3	US-08-346-147B-26 Sequence 26, Appli
C 17	15	78.9	404	3	US-08-497-214D-26 Sequence 26, Appli
C 18	15	78.9	1149	1	US-08-474-177-3 Sequence 3, Appli
C 19	15	78.9	1149	1	US-08-487-033-3 Sequence 3, Appli
C 20	15	78.9	1149	1	US-08-480-810-3 Sequence 3, Appli
C 21	15	78.9	1149	2	US-08-508-735-3 Sequence 3, Appli
C 22	15	78.9	1149	2	US-08-848-251-3 Sequence 3, Appli
C 23	15	78.9	1149	2	US-08-486-047-3 Sequence 3, Appli
C 24	15	78.9	1149	3	US-09-120-130-3 Sequence 3, Appli
C 25	15	78.9	1149	3	US-09-115-252-3 Sequence 3, Appli
C 26	15	78.9	1149	3	US-08-986-515-3 Sequence 3, Appli
C 27	15	78.9	1149	3	US-09-120-128-3 Sequence 3, Appli

28	15	78.9	1149	3	US-09-120-129-3	Sequence 3, Appli
29	15	78.9	1149	3	US-09-201-139-3	Sequence 3, Appli
30	15	78.9	1149	3	US-09-120-131-3	Sequence 3, Appli
31	15	78.9	36941	4	US-08-311-731A-130	Sequence 130, App
32	14.8	77.9	52	4	US-09-595-386-11	Sequence 11, Appl
C 33	14.8	77.9	228	4	US-08-750-088A-69	Sequence 69, Appl
C 34	14.8	77.9	306	3	US-09-147-935A-5	Sequence 5, Appli
C 35	14.8	77.9	306	3	US-09-147-935A-11	Sequence 11, Appl
C 36	14.8	77.9	306	3	US-09-147-935A-17	Sequence 17, Appl
C 37	14.8	77.9	306	3	US-09-147-935A-18	Sequence 18, Appl
C 38	14.8	77.9	306	3	US-09-147-935A-22	Sequence 22, Appl
C 39	14.8	77.9	306	3	US-09-147-935A-28	Sequence 28, Appl
C 40	14.8	77.9	306	3	US-09-147-935A-29	Sequence 29, Appl
C 41	14.8	77.9	306	3	US-09-147-935A-35	Sequence 35, Appl
C 42	14.8	77.9	306	3	US-09-147-935A-38	Sequence 38, Appl
C 43	14.8	77.9	319	4	US-08-750-088A-35	Sequence 35, Appl
C 44	14.8	77.9	324	4	US-08-750-088A-36	Sequence 36, Appl
C 45	14.8	77.9	418	4	US-09-072-596-302	Sequence 302, App

ALIGNMENTS

RESULT 1
US-07-960-389-1/c
Sequence 1, Application US/07960389
Patent No. 5705611
GENERAL INFORMATION:
APPLICANT: HAYASHIDA, Kasuhiro;
TITLE OF INVENTION: Human GM-CSF Receptor Component
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disc
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System Software 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/960,389
FILING DATE: 07-JAN-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 554,745
FILING DATE: 18-JUL-1990
APPLICATION NUMBER: PCT/US 91/04846
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bladale, John H. C.
REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DX0143Q
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2902
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3475 base pairs
TYPE: nucleotides
STRANDEDNESS: single
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: human
FEATURE:
OTHER INFORMATION: DNA sequence encoding Human GM-CSF receptor
US-07-960-389-1
Query Match 100.0%; Score 19; DB 1; Length 3475;
Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGTT 19
|||
Db 297 GGGTCTGCAGCGGATGTT 279

RESULT 2

US-09-252-991A-4370/c
; Sequence 4370, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4370
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4370

Query Match 86.3%; Score 16.4; DB 4; Length 1350;
Best Local Similarity 94.4%; Pred. No. 40;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTCTGCAGCGGATGTT 19
|||
Db 783 GGTCTGCAGCGGATGTT 766

RESULT 3

US-09-252-991A-4216
; Sequence 4216, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4216
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4216

Query Match 86.3%; Score 16.4; DB 4; Length 1455;
Best Local Similarity 94.4%; Pred. No. 40;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTCTGCAGCGGATGTT 19
|||
Db 709 GGTCTGCAGCGGATGTT 726

RESULT 4

US-09-341-587-4/c
; Sequence 4, Application US/09341587
; Patent No. 6346606

; GENERAL INFORMATION:
; APPLICANT: Mollenhauer, Jan
; TITLE OF INVENTION: Protein Containing an SRCR Domain
; FILE REFERENCE: 4121-108
; CURRENT APPLICATION NUMBER: US/09/341,587
; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: PCT/DE98/00096
; EARLIER FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5802
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-587-4

Query Match 86.3%; Score 16.4; DB 4; Length 5802;
Best Local Similarity 94.4%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGG 18
|||
Db 5435 GGGTCTGCAGCTGATGG 5418

RESULT 5

US-09-341-587-7/c
; Sequence 7, Application US/09341587
; Patent No. 6346606
; GENERAL INFORMATION:
; APPLICANT: Mollenhauer, Jan
; TITLE OF INVENTION: Protein Containing an SRCR Domain
; FILE REFERENCE: 4121-108
; CURRENT APPLICATION NUMBER: US/09/341,587
; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: PCT/DE98/00096
; EARLIER FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 28720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-587-7

Query Match 86.3%; Score 16.4; DB 4; Length 28720;
Best Local Similarity 94.4%; Pred. No. 48;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGG 18
|||
Db 28273 GGGTCTGCAGCTGATGG 28256

RESULT 6

US-09-252-991A-3819/c
; Sequence 3819, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3819
; LENGTH: 480
; TYPE: DNA

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3819

Query Match 81.1%; Score 15.4; DB 4; Length 480;
Best Local Similarity 94.1%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCTGCAGCGGATGG 18
DB 212 GGCTGCAGCGGATGG 196

RESULT 7

US-09-252-991A-3775/c
Sequence 3775, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3775
LENGTH: 897
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3775

Query Match 81.1%; Score 15.4; DB 4; Length 897;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCTGCAGCGGATGG 18
DB 681 GGCTGCAGCGGATGG 665

RESULT 8

US-09-252-991A-3591
Sequence 3591, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3591
LENGTH: 1272
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3591

Query Match 81.1%; Score 15.4; DB 4; Length 1272;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCTGCAGCGGATGG 18
DB 679 GGCTGCAGCGGATGG 695

RESULT 9
US-09-214-808-1/c
Sequence 1, Application US/09214808A
Patent No. 6475793

GENERAL INFORMATION:
APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
Patent No. 6475793
TITLE OF INVENTION: Plasmid
FILE REFERENCE: CARP0068
CURRENT APPLICATION NUMBER: US/09/214,808A
CURRENT FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: PCT/IB97/00950
PRIOR FILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 536165
TYPE: DNA
ORGANISM: Rhizobium
US-09-214-808-1

Query Match 81.1%; Score 15.4; DB 4; Length 536165;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GTCTGCAGCGGATGCT 19
DB 457877 GTCTGCAGCGGATGCT 457861

RESULT 10

US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 81.1%; Score 15.4; DB 3; Length 4403765;
Best Local Similarity 94.1%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATG 17
DB 4102066 GGGTCTGCAGCGGATG 4102082

RESULT 11

US-09-103-840A-1
Sequence 1, Application US/09103840A

Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 81.1%; Score 15.4; DB 3; Length 4411529;
Best Local Similarity 94.1%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATG 17
DB 4109869 GGGTGTGACGCGGATG 4109885

RESULT 12

US-08-581-918A-27
Sequence 27, Application US/08581918A
Patent No. 6043030

GENERAL INFORMATION:

APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-581-918A-27

Query Match 78.9%; Score 15; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGGA 15
DB 18 GGGTCTGCAGCGGGA 32

RESULT 13

US-08-346-147B-27
Sequence 27, Application US/08346147B
Patent No. 6211334

GENERAL INFORMATION:

APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,147B
FILING DATE: 29-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-346-147B-27

Query Match 78.9%; Score 15; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGGA 15
Db 18 GGGTCTGCAGCGGGA 32

RESULT 14
US-08-497-214D-27
Sequence 27, Application US/08497214D
Patent No. 6331390
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,214D
FILING DATE: 30-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET INFORMATION: MIV-071.05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-497-214D-27

Query Match 78.9%; Score 15; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGGA 15
Db 18 GGGTCTGCAGCGGGA 32

RESULT 15
US-08-581-918A-26
Sequence 26, Application US/08581918A
Patent No. 6043030
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-581-918A-26

Query Match 78.9%; Score 15; DB 3; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGA 15
DB 112 GGGTCTGCAGCGGA 126

RESULT 16
US-08-346-147B-26
Sequence 26, Application US/08346147B
Patent No. 6211334
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,147B
FILING DATE: 29-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299

TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-346-147B-26

Query Match 78.9%; Score 15; DB 3; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGA 15
DB 112 GGGTCTGCAGCGGA 126

RESULT 17
US-08-497-214D-26
Sequence 26, Application US/08497214D
Patent No. 6331390
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,214D
FILING DATE: 30-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
LENGTH: 404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-497-214D-26

Query Match 78.9%; Score 15; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGGA 15
|||||
Db 112 GGGTCTGCAGCGGGA 126

RESULT 18
US-08-474-177-3
Sequence 3, Application US/08474177
Patent No. 5624819
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..866
FEATURE:
NAME/KEY: CDS
LOCATION: 867..1016
FEATURE:
NAME/KEY: Intron
LOCATION: 1017..1149
US-08-474-177-3

Query Match 78.9%; Score 15; DB 1; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGGA 15
|||||
Db 1026 GGGTCTGCAGCGGGA 1040

RESULT 19
US-08-487-033-3
Sequence 3, Application US/08487033
Patent No. 5739027
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1E1-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-C
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..866
FEATURE:
NAME/KEY: CDS
LOCATION: 867..1016
FEATURE:
NAME/KEY: Intron
LOCATION: 1017..1149
US-08-487-033-3

Query Match 78.9%; Score 15; DB 1; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGTCTGCAGCGGA 15
Db 1026 GGGTCTGCAGCGGA 1040

RESULT 20

US-08-480-810-3
Sequence 3, Application US/08480810
Patent No. 5801236
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..866
FEATURE:
NAME/KEY: CDS
LOCATION: 867..1016
FEATURE:
NAME/KEY: Intron
LOCATION: 1017..1149
US-08-480-810-3

Query Match 78.9%; Score 15; DB 1; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGTCTGCAGCGGA 15
Db 1026 GGGTCTGCAGCGGA 1040

RESULT 21

US-08-508-735-3
Sequence 3, Application US/08508735
Patent No. 5843756
GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,735
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..866
FEATURE:
NAME/KEY: CDS
LOCATION: 867..1016
FEATURE:
NAME/KEY: Intron
LOCATION: 1017..1149
US-08-508-735-3

Query Match 78.9%; Score 15; DB 2; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCTGCGACGGGA 15
|||
Db 1026 GGGCTGCGACGGGA 1040

RESULT 22
US-08-848-251-3
Sequence 3, Application US/08848251
Patent No. 5989815
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..866
FEATURE:
NAME/KEY: CDS
LOCATION: 867..1016
FEATURE:
NAME/KEY: Intron
LOCATION: 1017..1149
US-08-848-251-3

Query Match 78.9%; Score 15; DB 2; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCTGCGACGGGA 15
|||
Db 1026 GGGCTGCGACGGGA 1040

RESULT 23
US-08-486-047-3
Sequence 3, Application US/08486047
Patent No. 5994095
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..866
FEATURE:
NAME/KEY: CDS
LOCATION: 867..1016
FEATURE:
NAME/KEY: intron
LOCATION: 1017..1149
US-08-486-047-3

Query Match      78.9%; Score 15; DB 2; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTCTGCAGCGGA 15
        |||||||
Db      1026 GGGTCTGCAGCGGA 1040

RESULT 24
US-09-120-130-3
; Sequence 3, Application US/09120130
; Patent No. 6037462
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,130
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,810
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..866
FEATURE:
NAME/KEY: CDS
LOCATION: 867..1016
FEATURE:
NAME/KEY: intron
LOCATION: 1017..1149
US-09-120-130-3

Query Match      78.9%; Score 15; DB 3; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTCTGCAGCGGA 15
        |||||||
Db      1026 GGGTCTGCAGCGGA 1040

RESULT 25
US-09-115-252-3
; Sequence 3, Application US/09115252
; Patent No. 6060301
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,252
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..866
FEATURE:
NAME/KEY: CDS
LOCATION: 867..1016
FEATURE:
NAME/KEY: Intron
LOCATION: 1017..1149
US-09-115-252-3

Query Match 78.9%; Score 15; DB 3; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCGACGCGGA 15
|||||
Db 1026 GGGTCGACGCGGA 1040

RESULT 26

US-08-986-515-3

Sequence 3, Application US/08986515

Patent No. 6090578

GENERAL INFORMATION:

APPLICANT: Kamb, Alexander

TITLE OF INVENTION: MT61 GENE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/986,515

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/480,810

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,938

FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,087

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,086

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,369

FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1149 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: 5'UTR

LOCATION: 1..866

FEATURE:

NAME/KEY: CDS

LOCATION: 867..1016

FEATURE:

NAME/KEY: Intron

LOCATION: 1017..1149

US-08-986-515-3

Query Match 78.9%; Score 15; DB 3; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCGACGGGA 15
| | | | | | | | | | | | | | | | | | | | | |
Db 1026 GGGTCGACGGGA 1040

RESULT 27

US-09-120-128-3
; Sequence 3, Application US/09120128
; Patent No. 6140473
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,128
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,047
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1149 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..866
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 867..1016
; FEATURE:
; NAME/KEY: Intron
; LOCATION: 1017..1149
; US-09-120-128-3

Query Match 78.9%; Score 15; DB 3; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCGACGGGA 15
| | | | | | | | | | | | | | | | | | | | | |
Db 1026 GGGTCGACGGGA 1040

RESULT 28

US-09-120-129-3
; Sequence 3, Application US/09120129
; Patent No. 6180776
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,129
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,047
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1149 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..866
FEATURE:
NAME/KEY: CDS
LOCATION: 867..1016
FEATURE:
NAME/KEY: Intron
LOCATION: 1017..1149
US-09-120-129-3

Query Match 78.9%; Score 15; DB 3; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGGA 15
|||
Db 1026 GGGTCTGCAGCGGGA 1040

RESULT 29
US-09-201-139-3
Sequence 3, Application US/09201139
Patent No. 6210949
GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,139
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/508,735
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..866
FEATURE:
NAME/KEY: CDS
LOCATION: 867..1016
FEATURE:
NAME/KEY: Intron
LOCATION: 1017..1149
US-09-201-139-3

Query Match 78.9%; Score 15; DB 3; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGGA 15
|||
Db 1026 GGGTCTGCAGCGGGA 1040

RESULT 30
US-09-120-131-3
Sequence 3, Application US/09120131
Patent No. 6218146
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,131
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,047
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300

;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1149 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: 5'UTR
;; LOCATION: 1..866
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 867..1016
;; FEATURE:
;; NAME/KEY: Intron
;; LOCATION: 1017..1149
US-09-120-131-3

Query Match 78.9%; Score 15; DB 3; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCTCTGACGGCGGA 15
Db 1026 GGGCTCTGACGGCGGA 1040

RESULT 31
US-08-311-731A-130
; Sequence 130, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311, 731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36941 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-130

Query Match 78.9%; Score 15; DB 4; Length 36941;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CTGACGGCGGATGT 19
Db 12443 CTGACGGCGGATGT 12457

RESULT 32
US-09-595-386-11
; Sequence 11, Application US/09595386
; Patent No. 6544792
; GENERAL INFORMATION:
; APPLICANT: Diaz-Torres, Maria
; TITLE OF INVENTION: Production of Secreted Polypeptides
; FILE REFERENCE: GC618
; CURRENT APPLICATION NUMBER: US/09/595,386
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: WO PCT/US99/31010
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-595-386-11

Query Match 77.9%; Score 14.8; DB 4; Length 52;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGCTGACGGCGGATGC 18
Db 3 GCGCTGACGGCGGATGC 20

RESULT 33
US-08-750-088A-69/c
; Sequence 69, Application US/08750088A
; Patent No. 6329138
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOWER, HANS
; APPLICANT: PORTAELS, FRAN OISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,088A
; FILING DATE: 21-FEB-1997


```

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657.0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-750-088A-69

Query Match      77.9%; Score 14.8; DB 4; Length 228;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGGTCTGCAGCGGATG 18
        |||||
Db      76 GGGTCTGCAGCGGATG 59

RESULT 34
US-09-147-935A-5/c
; Sequence 5, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 5
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-147-935A-5

Query Match      77.9%; Score 14.8; DB 3; Length 306;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGGTCTGCAGCGGATG 18
        |||||
Db      117 GGGTCTGCAGCGGATG 100

RESULT 35
US-09-147-935A-11/c
; Sequence 11, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
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; SEQ ID NO 11
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium chitae
US-09-147-935A-11

Query Match      77.9%; Score 14.8; DB 3; Length 306;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGGTCTGCAGCGGATG 18
        |||||
Db      117 GGGTCTGCAGCGGATG 100

RESULT 36
US-09-147-935A-17/c
; Sequence 17, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 17
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium genavense
US-09-147-935A-17

Query Match      77.9%; Score 14.8; DB 3; Length 306;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGGTCTGCAGCGGATG 18
        |||||
Db      117 GGGTCTGCAGCGGATG 100

RESULT 37
US-09-147-935A-18/c
; Sequence 18, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 18
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium goodii
US-09-147-935A-18

Query Match      77.9%; Score 14.8; DB 3; Length 306;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGGTCTGCAGCGGATG 18
```

Db 117 GGGTCTGCGCGGTGATGG 100

RESULT 38

US-09-147-935A-22/c
; Sequence 22, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 22
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium intracellulare
US-09-147-935A-22

Query Match 77.9%; Score 14.8; DB 3; Length 306;

Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGTCTGCGCGGTGATGG 18

Db 117 GGGTCTGCGCGGTGATGG 100

RESULT 39

US-09-147-935A-28/c
; Sequence 28, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 28
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium nonchromogenicum
US-09-147-935A-28

Query Match 77.9%; Score 14.8; DB 3; Length 306;

Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGTCTGCGCGGTGATGG 18

Db 117 GGGTCTGCGCGGTGATGG 100

RESULT 40

US-09-147-935A-29/c
; Sequence 29, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon

; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/0F425

; CURRENT APPLICATION NUMBER: US/09/147,935A

; CURRENT FILING DATE: 1999-03-19

; PRIOR APPLICATION NUMBER: PCT/KR98/00228

; PRIOR FILING DATE: 1998-07-28

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: KOPATIN 1.0

; SEQ ID NO 29

; LENGTH: 306

; TYPE: DNA

; ORGANISM: Mycobacterium paratuberculosis

US-09-147-935A-29

Query Match 77.9%; Score 14.8; DB 3; Length 306;

Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGTCTGCGCGGTGATGG 18

Db 117 GGGTCTGCGCGGTGATGG 100

Search completed: January 13, 2004, 17:58:34
Job time : 49.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2004, 15:53:18 ; Search time 744 Seconds
(without alignments)
1044.735 Million cell updates/sec

Title: US-09-719-737-9

Perfect score: 19

Sequence: 1 99gtctgcagcg9gatggt 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_vl:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
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- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	19	100.0	19	6	AX008655	AX008655 Sequence
2	19	100.0	19	6	AX008656	AX008656 Sequence
3	19	100.0	19	6	AX671168	AX671168 Sequence
C 4	19	100.0	19	6	AX671179	AX671179 Sequence
5	19	100.0	19	6	AX671180	AX671180 Sequence
C 6	19	100.0	2996	9	HUMGMC5FRB	M59941 Human GM-CS
C 7	19	100.0	86574	9	HS83387	AL008637 Human DNA
8	18	94.7	19	6	AX008657	AX008657 Sequence
9	18	94.7	19	6	AX008658	AX008658 Sequence
10	18	94.7	19	6	AX671169	AX671169 Sequence
11	18	94.7	19	6	AX671170	AX671170 Sequence
C 12	17.4	91.6	783	11	BV043795	BV043795 S212P6415
C 13	17.4	91.6	2711	10	CPU94688	U94688 Cavia porce
C 14	17.4	91.6	67292	2	AC120698_3	Continuation (4 of
C 15	17.4	91.6	86257	9	AL954650	AL954650 Human DNA
C 16	17.4	91.6	110000	2	AC120698_2	Continuation (3 of
C 17	17.4	91.6	142509	2	AC117942	AC117942 Tetradon
C 18	17.4	91.6	164532	2	AC116440	AC116440 Tetradon
C 19	17.4	91.6	177816	9	AC105219	AC105219 Homo sapi
C 20	17.4	91.6	200315	2	AC104885	AC104885 Mus muscu
21	17.4	91.6	246937	2	AC111254	AC111254 Rattus no
22	17	89.5	19	6	AX008662	AX008662 Sequence
23	17	89.5	19	6	AX671174	AX671174 Sequence
24	17	89.5	19	6	AX671181	AX671181 Sequence
25	17	89.5	19	6	AX671182	AX671182 Sequence
26	17	89.5	10225	1	AE004803	AE004803 Pseudomon
27	16.4	86.3	436	6	AX066133	AX066133 Sequence
C 28	16.4	86.3	778	9	AB02081540	AB020851 Homo sapi
C 29	16.4	86.3	1468	1	AB006797	AB006797 Pseudomon
30	16.4	86.3	1824	6	AX120193	AX120193 Sequence
31	16.4	86.3	1947	6	BD162310	BD162310 Novel pol
32	16.4	86.3	2097	9	BC015649	BC015649 Homo sapi
C 33	16.4	86.3	4690	1	MLCPMOA	L40804 Methylococc
C 34	16.4	86.3	5802	6	A90822	A90822 Sequence 1
C 35	16.4	86.3	5802	6	AR193170	AR193170 Sequence
C 36	16.4	86.3	5802	6	BD064963	BD064963 Protein c
C 37	16.4	86.3	5802	9	HSDMBT1	AJ000342 Homo sapi
C 38	16.4	86.3	7080	1	MCU94337	U94337 Methylococc
C 39	16.4	86.3	7656	9	HS243224	AJ243224 Homo sapi
C 40	16.4	86.3	7683	9	HS243212	AJ243212 Homo sapi
C 41	16.4	86.3	7686	9	AF159456	AF159456 Homo sapi
C 42	16.4	86.3	10171	1	AE004704	AE004704 Pseudomon
C 43	16.4	86.3	10698	1	AE005902	AE005902 Caulobact
C 44	16.4	86.3	12239	1	AE012048	AE012048 Xanthomon
C 45	16.4	86.3	12239	1	AE012048	AE012048 Xanthomon

ALIGNMENTS

RESULT 1
AX008655/c 19 bp DNA linear PAT 06-SEP-2000
LOCUS AX008655 Sequence 8 from Patent WO9966037.
DEFINITION AX008655
ACCESSION AX008655
VERSION AX008655.1 GI:9996179
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
AUTHORS Renzl, P.
TITLE Antisense oligonucleotides for treating or preventing atopic
diseases and neoplastic cell proliferation
JOURNAL Patent: WO 9966037-A 8 23-DEC-1999;

RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES
Source
1. .19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sense oligonucleotide for IL-3, IL-5 and GM-CSF"

BASE COUNT 4 a 10 c 3 g 2 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGTCTGCAGCGGATGCT 19
Db 19 GGGTCTGCAGCGGATGCT 1

RESULT 2
AX008656 19 bp DNA linear PAT 06-SEP-2000
LOCUS
DEFINITION Sequence 9 from Patent WO9966037.
ACCESSION AX008656
VERSION AX008656.1 GI:9996180
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Renzi, P.
TITLE Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
JOURNAL Patent: WO 9966037-A 9 23-DEC-1999;
RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES
Source
1. .19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide inhibiting the common subunit of IL-3, IL-5 and GM-CSF human receptor"

BASE COUNT 2 a 3 c 10 g 4 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGTCTGCAGCGGATGCT 19
Db 1 GGGTCTGCAGCGGATGCT 19

RESULT 3
AX671168 19 bp DNA linear PAT 27-MAR-2003
LOCUS
DEFINITION Sequence 8 from Patent WO03004511.
ACCESSION AX671168
VERSION AX671168.1 GI:29329624
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Renzi, P., Allam, M. and Allakhverdi, Z.
TITLE Methods for increasing in vivo efficacy of oligonucleotides and inhibiting inflammation in mammals
JOURNAL Patent: WO 03004511-A 8 16-JAN-2003;
Topigen Pharmaceuticals Inc (CA)
FEATURES
Source
1. .19
/organism="synthetic construct"

/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sequence is completely synthesized"

BASE COUNT 2 a 3 c 10 g 4 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGTCTGCAGCGGATGCT 19
Db 1 GGGTCTGCAGCGGATGCT 19

RESULT 4
AX671179/c 19 bp DNA linear PAT 27-MAR-2003
LOCUS
DEFINITION Sequence 19 from Patent WO03004511.
ACCESSION AX671179
VERSION AX671179.1 GI:29329635
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Renzi, P., Allam, M. and Allakhverdi, Z.
TITLE Methods for increasing in vivo efficacy of oligonucleotides and inhibiting inflammation in mammals
JOURNAL Patent: WO 03004511-A 19 16-JAN-2003;
Topigen Pharmaceuticals Inc (CA)
FEATURES
Source
1. .19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sequence is completely synthesized"

BASE COUNT 4 a 10 c 3 g 2 t
ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGTCTGCAGCGGATGCT 19
Db 19 GGGTCTGCAGCGGATGCT 1

RESULT 5
AX671180 19 bp DNA linear PAT 27-MAR-2003
LOCUS
DEFINITION Sequence 20 from Patent WO03004511.
ACCESSION AX671180
VERSION AX671180.1 GI:29329636
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Renzi, P., Allam, M. and Allakhverdi, Z.
TITLE Methods for increasing in vivo efficacy of oligonucleotides and inhibiting inflammation in mammals
JOURNAL Patent: WO 03004511-A 20 16-JAN-2003;
Topigen Pharmaceuticals Inc (CA)
FEATURES
Source
1. .19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sequence is completely synthesized"

BASE COUNT 2 a 3 c 10 g 4 t
ORIGIN


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repeat_region /clone="CTA-833B7"
/clone_11b="CIT978SK-A2"
1..176
/note="AluSp repeat: matches 138. .313 of consensus"
repeat_region 211..220
/note="2.0 copies 5 mer GAAAA 20% conserved"
repeat_region 235..249
/note="2.5 copies 6 mer CCGGCC 30% conserved"
repeat_region 239..258
/note="20.0 copies 1 mer C 22% conserved"
repeat_region 627..636
/note="2.5 copies 4 mer TCCC 20% conserved"
repeat_region 642..653
/note="4.0 copies 3 mer AGA 24% conserved"
repeat_region /note="MIR repeat: matches 212. .254 of consensus"
1072..1084
/note="2.6 copies 5 mer GGAGA 26% conserved"
repeat_region 1163..1173
/note="2.2 copies 5 mer GGGAT 22% conserved"
repeat_region /note="complement(1233. .1462)"
/note="L2 repeat: matches 2418. .2653 of consensus"
1791..2095
/note="AluX repeat: matches 1. .307 of consensus"
2521..2537
/note="4.2 copies 4 mer CTCC 25% conserved"
repeat_region 2866..2881
/note="2.0 copies 8 mer GAGGAGG 32% conserved"
2902..2911
/note="2.5 copies 4 mer GGAG 20% conserved"
3263..3277
/note="2.1 copies 7 mer CTCACC 30% conserved"
3359..3522
/note="MER58A repeat: matches 43. .207 of consensus"
3532..3838
/note="AluX repeat: matches 1. .308 of consensus"
/note="complement(3872. .3956)"
repeat_region /note="MLTJ2 repeat: matches 366. .450 of consensus"
complement(4030. .4288)
/note="MLTJ repeat: matches 1. .261 of consensus"
complement(4478. .4555)
/note="MIR repeat: matches 64. .143 of consensus"
4592..4609
/note="3.0 copies 6 mer CTGGGG 27% conserved"
complement(4645. .5195)
/note="LTR50 repeat: matches 4. .766 of consensus"
5291..5370
/note="LIME1 repeat: matches 5523. .5604 of consensus"
complement(5371. .5676)
/note="AluX repeat: matches 1. .310 of consensus"
5677..6268
/note="LIME1 repeat: matches 5604. .6332 of consensus"
6302..6481
/note="L2 repeat: matches 2636. .2819 of consensus"
complement(6483. .6755)
/note="MER15 repeat: matches 393. .688 of consensus"
6934..6962
/note="2.1 copies 14 mer TGCATGTATGCA 49% conserved"
6944..6953
/note="2.5 copies 4 mer TGCA 20% conserved"
6984..7002
/note="1.9 copies 10 mer TGCAAGGTGTG 29% conserved"
6999..7085
/note="6.2 copies 14 mer GTGTATGTACAT 66% conserved"
7000..7014
/note="2.5 copies 6 mer TGTACA 30% conserved"
7006..7022
/note="2.1 copies 8 mer TGTACATG 25% conserved"
7047..7193
/note="6.1 copies 24 mer GTGTGATGTATATGTGCTGC 113% conserved"
7048..7080
/note="5.5 copies 6 mer TGTGTA 30% conserved"
```

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repeat_region 7053..7085
/note="4.1 copies 8 mer ATGTGTAT 29% conserved"
repeat_region 7118..7127
/note="2.5 copies 4 mer TGCA 20% conserved"
repeat_region 7125..7136
/note="2.0 copies 6 mer ATGTGT 24% conserved"
repeat_region 7148..7164
/note="2.8 copies 6 mer TGTGTA 25% conserved"
repeat_region 7203..7332
/note="L2 repeat: matches 3165. .3313 of consensus"
7333..7342
/note="2.5 copies 4 mer GAAT 20% conserved"
7347..7532
/note="MIR repeat: matches 2. .191 of consensus"
complement(7537. .7640)
/note="MIR repeat: matches 158. .262 of consensus"
complement(8152. .8228)
/note="MIR repeat: matches 184. .260 of consensus"
8253..8341
/note="L2 repeat: matches 3214. .3311 of consensus"
8504..8516
/note="2.6 copies 5 mer AGAGA 26% conserved"
8848..8859
/note="2.0 copies 6 mer AGTTCC 24% conserved"
9588..9602
/note="5.0 copies 3 mer GCA 21% conserved"
9920..9935
/note="2.0 copies 8 mer TTGGGGG 32% conserved"
10303..10313
/note="2.2 copies 5 mer ACACA 22% conserved"
10428..10439
/note="3.0 copies 4 mer TGCT 24% conserved"
10570..10580
/note="2.2 copies 5 mer TTTC 22% conserved"
complement(11386. .11858)
/note="L2 repeat: matches 2722. .3312 of consensus"
11913..29288
/gene="NCF4"
join(11913. .12573,15415. .15499,16289. .16442,18762. .18832,
21785. .21912,23022. .23079,23697. .23795,27023. .27153,
27399. .27464,28998. .29288)
/product="bK833B7.1 (neutrophil cytosolic factor 4 (40kD))"
/note="match: CDNA8: Em:AB002665 Em:X77094 Em:U59488
match: ESTs: Em:AA177839 Em:A1007048 Em:AA465462
Em:AA465389 Em:AA485518 Em:A1381940 Em:AA744805
Em:AA975113 Em:AA969460 Em:AA948430 Em:A1435296
Em:A1299103 Em:AA648472 Em:AA702857 Em:A1088359 Em:D20144
Em:AA909156 Em:AA688071 Em:W95229 Em:A1439568"
/evidence="not_experimental"
complement(11982. .12109)
/note="L2 repeat: matches 2918. .3064 of consensus"
12358..12367
/note="3.3 copies 3 mer GGA 20% conserved"
12443..12453
/note="2.2 copies 5 mer GAGAC 22% conserved"
join(12542. .12573,15415. .15499,16289. .16442,18762. .18832,
21785. .21912,23022. .23079,23697. .23795,27023. .27153,
27399. .27464,28998. .29193)
/gene="NCF4"
/note="match: proteins: Tr:O60808 Tr:P97369"
/codon_start=1
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Query Match 100.0%; Score 19; DB 9; Length 86574;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCTGACGCGGATGTT 19
DB 74634 GGGCTGACGCGGATGTT 74616

RESULT 8
AX008657
LOCUS AX008657 19 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 10 from Patent WO966037.
ACCESSION AX008657
VERSION AX008657.1 GI:9996181
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Renzi, P.
TITLE Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
JOURNAL Patent: WO 9966037-A 10 23-DEC-1999;
RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide inhibiting the common subunit of IL-3, IL-5 and GM-CSF human receptor"

BASE COUNT 2 a 3 c 9 g 5 t
ORIGIN

Query Match 94.7%; Score 18; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGTCTGCAGCGGATGCT 19
Db 1 GGTCTGCAGCGGATGCT 18

RESULT 9
AX008658
LOCUS AX008658 19 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 11 from Patent WO966037.
ACCESSION AX008658
VERSION AX008658.1 GI:9996182
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Renzi, P.
TITLE Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation
JOURNAL Patent: WO 9966037-A 11 23-DEC-1999;
RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide inhibiting the common subunit of IL-3, IL-5 and GM-CSF human receptor"

BASE COUNT 3 a 3 c 10 g 3 t
ORIGIN

Query Match 94.7%; Score 18; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTCTGCAGCGGATGCT 18
Db 2 GGTCTGCAGCGGATGCT 19

RESULT 10
AX671169
LOCUS AX671169 19 bp DNA linear PAT 27-MAR-2003

DEFINITION Sequence 9 from Patent WO03004511.
ACCESSION AX671169
VERSION AX671169.1 GI:29329625
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Renzi, P., Allam, M. and Allakhverdi, Z.
TITLE Methods for increasing in vivo efficacy of oligonucleotides and inhibiting inflammation in mammals
JOURNAL Patent: WO-03004511-A 9 16-JAN-2003;
Topigen Pharmaceuticals Inc (CA)
FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sequence is completely synthesized"

BASE COUNT 2 a 3 c 9 g 5 t
ORIGIN

Query Match 94.7%; Score 18; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGTCTGCAGCGGATGCT 19
Db 1 GGTCTGCAGCGGATGCT 18

RESULT 11
AX671170
LOCUS AX671170 19 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 10 from Patent WO03004511.
ACCESSION AX671170
VERSION AX671170.1 GI:29329626
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Renzi, P., Allam, M. and Allakhverdi, Z.
TITLE Methods for increasing in vivo efficacy of oligonucleotides and inhibiting inflammation in mammals
JOURNAL Patent: WO 03004511-A 10 16-JAN-2003;
Topigen Pharmaceuticals Inc (CA)
FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sequence is completely synthesized"

BASE COUNT 3 a 3 c 10 g 3 t
ORIGIN

Query Match 94.7%; Score 18; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTCTGCAGCGGATGCT 18
Db 2 GGTCTGCAGCGGATGCT 19

RESULT 12
BV043795/c
LOCUS BV043795 783 bp DNA linear STS 31-MAY-2003
DEFINITION S212P6415FA10.T0 CZECHII/E1 Mus musculus STS genomic, sequence tagged site.
ACCESSION BV043795
VERSION BV043795.1 GI:31159590
KEYWORDS STS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 783)
Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C., Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
The mosaic structure of variation in the laboratory mouse genome
JOURNAL Nature 420 (6915), 574-578 (2002)
MEDLINE 22354684
PUBMED 12466852
COMMENT
Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome Research
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172521477
Fax: 6172580903
Email: kersti@genome.wi.mit.edu
Primer A: None
Primer B: None
STS size: 783
Protocol:
WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 12S1/SvimJ, C3H/HeJ, and BALB/cByJ. The WGS reads were placed uniquely on the MGSv3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were annotated
as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.
FEATURES
Source
1. .783
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CZECHII/EI"
/db_xref="taxon:10090"
/map="16 40-713 30321911-30322586"
/clone_11b="CZECHII/EI"
<1. .>783
BASE COUNT 180 a 202 c 199 g 201 t 1 others
ORIGIN
Query Match 91.6%; Score 17.4; DB 11; Length 783;
Best Local Similarity 94.7%; Pred. No. 7.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGTCTGCAGCGGATGCT 19
|||||
Db 568 GGGCCTGCAGCGGATGCT 550
RESULT 13
CPU94688/c 2711 bp mRNA linear ROD 16-NOV-1998
LOCUS Cavia porcellus interleukin-5 receptor beta chain (IL5) mRNA, complete cds.
ACCESSION U94688
VERSION U94688
KEYWORDS U94688.1 GI:3882357
SOURCE Cavia porcellus (domestic guinea pig)
ORGANISM Cavia porcellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
REFERENCE 1 (bases 1 to 2711)
Logsdon, N.J., Graham, A. and Scott, C.W.
TITLE Guinea pig IL5 receptor beta chain
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 2711)
Logsdon, N.J., Graham, A. and Scott, C.W.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Target Discovery, Zeneca Pharmaceuticals, 1800 Concord Pike, Wilmington, DE 19850-5437, USA

FEATURES
Source
Location/Qualifiers
1. .2711
/organism="Cavia porcellus"
/mol_type="mRNA"
/db_xref="taxon:10141"
/cell_type="bronchial alveolar lavage cells"
1. .2711
/gene="IL5"
17. .2689
/gene="IL5"
/codon_start=1
/product="interleukin-5 receptor beta chain"
/protein_id="AAC77520.1"
/db_xref="GI:3882358"
/translation="MAPRPGILLMALLLCRGPRVGESEDTVPLQTLRCYNDYTSRIVCSWAEEAAEQILNVTLLHRRLKSNHSEAVSCETEDMPMSHCPSPCVRRACVITYTAFALADNDYVSFEEDRPLDRLTWTLOHQVQPPPODVOINTSGDOVLTWVALEGPHTSWLSQRDLFEVYKRLHEPWESASTLHNSQAALGPELFLPSSITYVARVTRLARGSGFSGRPSQWSPVSSQPDQAOQVDFDGAFTLSCWVRSQVTSVSGFGLFRRSLDAGEQECPOVQKEELHDIYTRHSCQIRVSNPRHSQYTVTRPENGKEFTRSANHIQMAPLTLNVTXGDYTSLRWTEKMYSHIENTFEIQRTAGDRWNSKTE TLKNAHNMPLPPEPATYTLARVRKPSPGGAYNGIWSWSEQRWTTDMALPTVLA LVLVLTALLALLRFGCLYGRYLRNKKWKEKIPNSKSHLFKNGSAGRLPDSRMFA SRSAPSWGVRGFLIEGVCPADSRDSEVSPITTEDPTVCDPSPSEPHSTPAASDLT QEQPSPVQPGRPVQDQPDQDQATPDENGPLYGPBPHSHSLPDLAGQQGPKPLPGSLE YLCLPGRGAQVPLPAQGAQPAEGCLSGEVTQGSPLYLAGGPPAPDPGSOA QGPGDGRGDSPVILPTNSGPRHPVAVSGYTTADIALTLTSSAVSLAPDPLCPG LSDEAPAPPTPGKPRFEGYVELPASMGPLPKSFLGGFVPPAPSSPVLSPTGQDVSP LSPAPRGLVLDQVGDYCFLLPGISGGLSPRSKPSVPVPCPELMDIEQFVKKPFGQ PMPQVPAIQFERSLKKQDYLTLPWEVSRPHCYC"
BASE COUNT 513 a 940 c 777 g 481 t
ORIGIN
Query Match 91.6%; Score 17.4; DB 10; Length 2711;
Best Local Similarity 94.7%; Pred. No. 6.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGTCTGCAGCGGATGCT 19
|||||
Db 113 GGGTCTGCAGCGGACGCT 95
RESULT 14
AC120698 3/c
WPCOMMENT
Sequence split into 4 fragments LOCUS AC120698 Accession AC120698
Fragment Name Begin End
AC120698_0 1 110000
AC120698_1 100001 210000
AC120698_2 200001 310000
AC120698_3 300001 367292
Continuation (4 of 4) of AC120698 from base 300001 (AC120698 Rattus norvegicus clone CH2:
Query Match 91.6%; Score 17.4; DB 2; Length 67292;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGTCTGCAGCGGATGCT 19
|||||
Db 2383 GGGTCTGCAGCGGATGAT 2365
RESULT 15
AL954650/c 86257 bp DNA linear PRI 26-FEB-2003
LOCUS Human DNA sequence from clone RP11-523M19 on chromosome 1, complete sequence.
DEFINITION AL954650
ACCESSION AL954650
VERSION AL954650.8 GI:28564367
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 86257)
Martin, S.
Direct Submission
Submitted (25-FEB-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Feb 25, 2003 this sequence version replaced gl:28208053.

COMMENT

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human

chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr1>

RP11-523M19 is from the library RPCI-11.2 constructed by the group

of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6.

FEATURES

SOURCE

Location/Qualifiers
1..86257
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-523M19"
/clone_1b="RPCI-11.2"

BASE COUNT 29602 a 13951 c 14808 g 27896 t
ORIGIN

Query Match 91.6%; Score 17.4; DB 9; Length 86257;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCTGCAGCGGATGCT 19
|||||||
Db 59984 GGGCTGCAGCAGATGCT 59966

RESULT 16

AC120698 2/c

WPCOMMENT

Sequence split into 4 fragments LOCUS AC120698 Accession AC120698

Fragment Name	Begin	End
AC120698_0	1	110000
AC120698_1	100001	210000
AC120698_2	200001	310000
AC120698_3	300001	367292

Continuation (3 of 4) of AC120698 from base 200001 (AC120698 Rattus norvegicus clone CH2

Query Match 91.6%; Score 17.4; DB 2; Length 110000;

Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCTGCAGCGGATGCT 19
|||||||
Db 102383 GGGCTGCAGCGGATGAT 102365

RESULT 17

AC117942/c

LOCUS

DEFINITION

AC117942 142509 bp DNA linear HTG 05-SEP-2002
Tetraodon nigroviridis clone GSTNB-27D21, WORKING DRAFT SEQUENCE, 4
ordered pieces.

ACCESSION

AC117942 GI:22725952

HTG: HTGS_PHASE2; HTGS_DRAFT.

KEYWORDS

SOURCE

ORGANISM

Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

AUTHORS

1 (bases 1 to 142509)
Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,
Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karins, E.,
Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,
Margulies, E.H., Masello, C., Maskeri, B., Mastrian, S.D.,
McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R.,
Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schueler, M.G., Sison, C.,
Stantrop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,
Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
NISC Comparative Sequencing Initiative

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Direct Submission
Submitted (05-SEP-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Sep 5, 2002 this sequence version replaced gl:20136917.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc.zoo@hgrl.nih.gov
----- Project Information
Center project name: cvg
Center clone name: 027D21

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 141403 bases at least Q40
Consensus quality: 141846 bases at least Q30

Consensus quality: 142063 bases at least Q20
Insert size: 12900; agarose-fp
Insert size: 142209; sum-of-contigs
Quality coverage: 10.93x in Q20 bases; agarose-fp
Quality coverage: 9.92x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 19429: contig of 19429 bp in length
* 19430 19529: gap of unknown length
* 19530 107773: contig of 88244 bp in length
* 107774 107873: gap of unknown length
* 107874 131292: contig of 23419 bp in length
* 131293 131392: gap of unknown length
* 131393 142509: contig of 1117 bp in length.
Location/Qualifiers
1. 142509
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="GSTNB-27D21"
/clone_lib="GSTNB"
/note="Genoscope designation: COAB027D21"
1. 19429
/note="assembly_fragment"
clone_end:T7
vector_side:left"
19530. 107773
/note="assembly_fragment"
107874. 131292
/note="assembly_fragment"
118928. 142509
/note="clone overlaps with GenBank Accession Number
AC116440 clone GSTNA-49N2 (center project name cvf)"
131393. 142509
/note="assembly_fragment"
clone_end:SP6
vector_side:right"

BASE COUNT 34414 a 35682 c 34612 g 37501 t 300 others
ORIGIN

Query Match 91.6%; Score 17.4; DB 2; Length 142509;
Best Local Similarity 94.7%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGCTCTGACGGGATGCT 19
|||||
Db 134729 GGCTCTGACGGGACGCT 134711

RESULT 18
AC116440/c
LOCUS
DEFINITION
AC116440 164532 bp DNA linear HTG 23-OCT-2002
Tetraodon nigroviridis clone GSTNA-49N2, WORKING DRAFT SEQUENCE, 6
ordered pieces.
AC116440
AC116440
VERSION AC116440.3 GI:24270692
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1 (bases 1 to 164532)
REFERENCE
1 Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Cariaga, K., Coleman, B., Dietrich, N.L., Engle, J., Granite, S.,
Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L.,
Idol, J.R., Karlins, E., Laric, P., Lee-Jin, S.-Q., Legaapi, R.,
Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B.,
Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C.,
Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K.,
Schueler, M.G., Sison, C., Stantirip, S., Thomas, J.W., Thomas, P.J.,
Touchman, J.W., Vogt, J.L., Walker, M., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 164532)
Green, E.D.
Direct Submission
Submitted (28-MAR-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gathersburg, MD 20877, USA
3 (bases 1 to 164532)
Green, E.D.
Direct Submission
Submitted (23-OCT-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gathersburg, MD 20877, USA
On Oct 23, 2002 this sequence version replaced gi:21465411.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc_zoo@nhgri.nih.gov
----- Project Information
Center project name: cvf
Center clone name: 049N02

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid, n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 163158 bases at least Q40
Consensus quality: 163658 bases at least Q30
Consensus quality: 163904 bases at least Q20
Insert size: 106000; agarose-fp
Insert size: 164032; sum-of-contigs
Quality coverage: 15.47x in Q20 bases; agarose-fp
Quality coverage: 10.00x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 12551: contig of 12551 bp in length
* 12552 12651: gap of unknown length
* 12652 67722: contig of 55071 bp in length
* 67723 67822: gap of unknown length
* 67823 87024: contig of 19202 bp in length
* 87025 87124: gap of unknown length
* 87125 92799: contig of 5675 bp in length
* 92800 92899: gap of unknown length

FEATURES

Source

1. 164532
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone_lib="GSTNA-49N2"
/clone_1ib="GSTNA"
/note="Genoscope designation: COAA049N02"

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1. .24382
/note="clone overlaps with GenBank Accession Number AC117942 clone GSTNB-27D21 (center project name cvq)"

misc_feature
1. .12551
/note="assembly_fragment
clone_end:T7
vector_side:left"
12652. .67722
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67823. .87024
/note="assembly_fragment"
87125. .92799
/note="assembly_fragment"
92900. .144325
/note="assembly_fragment"
144426. .164532
/note="assembly_fragment
clone_end:SP6
vector_side:right"

BASE COUNT 39575 a 41275 c 41473 g 41709 t 500 others

ORIGIN

Query Match 91.6%; Score 17.4; DB 2; Length 164532;
Best Local Similarity 94.7%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 GGGTCTGCAGCGGATGCT 19
|||||
Db 16602 GGGTCTGCAGCGGATGCT 16584

RESULT 19
AC105219 177816 bp DNA linear PRI 30-SEP-2002
LOCUS AC105219
DEFINITION Homo sapiens chromosome 8, clone RP11-429J17, complete sequence.
ACCESSION AC105219
VERSION AC105219.6 GI:23379185
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 177816)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazeares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Margis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPeeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,

Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (26-DEC-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 177816)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (09-SEP-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 177816)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (30-SEP-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 30, 2002 this sequence version replaced gi:22759307.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L23081
Center clone name: 429_J_17

FEATURES

Source

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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"

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/clone_lib="RPC1-11 Human Male BAC"
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/rpt_family="L2"
repeat_region complement(1950..2022)
/rpt_family="MIR"
repeat_region complement(2052..2362)
/rpt_family="AluSx"
repeat_region complement(2382..2491)
/rpt_family="FLAM_C"
repeat_region 3029..3268
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repeat_region 3929..3992
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repeat_region 13252..13285
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repeat_region 13358..13413
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repeat_region 19441..19445
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repeat_region 20044..20107
/rpt_family="(GGA)n"
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repeat_region complement(28420..28556)
/rpt_family="LIM4"
repeat_region 29100..29192
/rpt_family="MIR"
repeat_region complement(29575..29720)
/rpt_family="LIMC5"
repeat_region complement(29883..30138)
/rpt_family="LIMC4a"
repeat_region 30197..30314
/rpt_family="FLAM_A"
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/rpt_family="LIMC4"
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repeat_region 42633..42770
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repeat_region 42771..43069
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/rpt_family="AluJb"
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repeat_region 43718..43900
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repeat_region 43903..44255
/rpt_family="MLT1I"
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/rpt_family="MLT1I"
repeat_region 44766..45629
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Query Match 91.6%; Score 17.4; DB 9; Length 177816;
Best Local Similarity 94.7%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GGGTCTGCAGCGGATGCT 19
Db 128432 GGGTCTGCAGCTGATGCT 128450
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RESULT 20
AC104885/c
LOCUS
DEFINITION Mus musculus clone RP23-125P19, WORKING DRAFT SEQUENCE, 6 ordered
pieces.
AC104885
AC104885.3 GI:24182334
VERSION AC104885.3
KEYWORDS HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 200315)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP23-125P19
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 200315)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campiano,A., Chang,J., Chararo,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
McClellan,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
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TITLE Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
JOURNAL Direct Submission
REFERENCE Submitted (22-DEC-2001) Whitehead Institute/MIT Center for Genome
AUTHORS Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 200315)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kelle,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Maclean,C., MacDonald,P., Major,J.,
Mathews,C., McCarthy,M., Meldrim,J., Menus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,
Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission

TITLE Submitted (21-OCT-2002) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Oct 21, 2002 this sequence version replaced g1:19881860.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L18985
Center clone name: 125_P_19
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 199225 bases at least Q40
Consensus quality: 199503 bases at least Q30
Consensus quality: 199621 bases at least Q20
Insert size: 19300; agarose-fp
Insert size: 199815; sum-of-contigs
Quality coverage: 10.8 in Q20 bases; agarose-fp
Quality coverage: 10.4 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 36019: contig of 36019 bp in length
* 36020 36119: gap of 100 bp
* 36120 51874: contig of 15755 bp in length
* 51875 51974: gap of 100 bp
* 51975 75930: contig of 23956 bp in length
* 75931 76030: gap of 100 bp
* 76031 104917: contig of 28887 bp in length
* 104918 105017: gap of 100 bp
* 105018 178310: contig of 73293 bp in length
* 178311 178410: gap of 100 bp
* 178411 200315: contig of 21905 bp in length.
Location/Qualifiers
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/organism="Mus musculus"

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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-125P19"
/clone_lib="RPCI-23 Female Mouse BAC"
1..36019
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clone_end:SP6
vector_side:left"
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76031..104917
/note="assembly_fragment"
105018..178310
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178411..200315
/note="assembly_fragment
clone_end:T7
vector_side:right"
BASE COUNT 53188 a 46038 c 47231 g 53356 t 502 others
ORIGIN
Query Match 91.6%; Score 17.4; DB 2; Length 200315;
Best Local Similarity 94.7%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGTCTGACGGGATGCT 19
||| ||||| ||||| |||||
Db 154350 GGGCTTCGACGGGATGCT 154332
RESULT 21
AC111254
LOCUS
DEFINITION Rattus norvegicus clone CH230-32J17, *** SEQUENCING IN PROGRESS
AC111254
AC111254 246937 bp DNA linear HTG 13-MAY-2003
AC111254.4 GI:30578635
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 246937)
Muzny,D,Marie, Metzker,M,lee, Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Caesar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Derram,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,S., Hladun,S.L., Hodgson,A., Hognes,M.,
Hollins,B., Howells,S., Huliyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorenshewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,

Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okunolu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Unpublished
2 (bases 1 to 246937)

Worley, K.C.
Direct Submission
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 246937)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23269171.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GLWX
Center clone name: CH230-32J17
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 232316 bases at least Q40
Consensus quality: 236042 bases at least Q30
Consensus quality: 238624 bases at least Q20
Estimated insert size: 248705; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
* be preserved.
* 1 235507: contig of 235507 bp in length
* 235508 235607: gap of unknown length
* 235608 236672: contig of 1065 bp in length
* 236673 236772: gap of unknown length
* 236773 237819: contig of 1047 bp in length
* 237820 237919: gap of unknown length
* 237920 240534: contig of 2615 bp in length
* 240535 240634: gap of unknown length
* 240635 242760: contig of 2126 bp in length
* 242761 242860: gap of unknown length
* 242861 246937: contig of 4077 bp in length.
location/Qualifiers
1. 246937
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-32J17"
1. 1422
/note="wgs_contig"
misc_feature 232662..235507
misc_feature /note="wgs_contig"
BASE COUNT 67730 a 56226 c 53928 g 62488 t 6565 others
ORIGIN

Query Match 91.6%; Score 17.4; DB 2; Length 246937;
Best Local Similarity 94.7%; Pred. No. 3.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGTCGACGCGGATGCT 19
|||||
Db 105519 GGGTCGACGCGGATGCT 105537
|||||

RESULT 22
AX008662 19 bp DNA linear PAT 06-SEP-2000
LOCUS
DEFINITION Sequence 15 from Patent WO9966037.
ACCESSION AX008662
VERSION AX008662.1 GI:9996186
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 Renzi, P.
Antisense oligonucleotides for treating or preventing atopic
diseases and neoplastic cell proliferation
Patent: WO 9966037-A 15 23-DEC-1999;
JOURNAL RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
location/Qualifiers
1. 19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide inhibiting the common
subunit of IL-3, IL-5 and GM-CSF human receptor"
FEATURES
source
1. 19
/organism="synthetic construct"
BASE COUNT 2 a 3 c 8 g 6 t
ORIGIN

Query Match 89.5%; Score 17; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GTCTGACGCGGATGCT 19
|||||
Db 1 GTCTGACGCGGATGCT 17
|||||

RESULT 23
AX671174 19 bp DNA linear PAT 27-MAR-2003
LOCUS AX671174

DEFINITION Sequence 14 from Patent WO03004511.
ACCESSION AX671174
VERSION AX671174.1 GI:29329630
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Renzi, P., Allam, M. and Allakhverdi, Z.
TITLE Methods for increasing in vivo efficacy of oligonucleotides and
inhibiting inflammation in mammals
JOURNAL Patent: WO 03004511-A 14 16-JAN-2003;
Topigen Pharmaceuticals Inc (CA)
FEATURES
source location/Qualifiers
1. 19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sequence is completely synthesized"
BASE COUNT 2 a 3 c 8 g 6 t
ORIGIN
Query Match 89.5%; Score 17; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 3 GTCTGCAGCGGATGCT 19
|||||
Db 1 GTCTGCAGCGGATGCT 17
RESULT 24
AX671181 19 bp DNA linear PAT 27-MAR-2003
LOCUS
DEFINITION Sequence 21 from Patent WO03004511.
ACCESSION AX671181
VERSION AX671181.1 GI:29329637
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Renzi, P., Allam, M. and Allakhverdi, Z.
TITLE Methods for increasing in vivo efficacy of oligonucleotides and
inhibiting inflammation in mammals
JOURNAL Patent: WO 03004511-A 21 16-JAN-2003;
Topigen Pharmaceuticals Inc (CA)
FEATURES
source location/Qualifiers
1. 19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sequence is completely synthesized"
misc_feature 9
/note="N corresponds to 2,6-diaminopurine nucleoside
(DAP)"
misc_feature 15
/note="N corresponds to 2,6-diaminopurine nucleoside
(DAP)"
BASE COUNT 0 a 3 c 10 g 4 t 2 others
ORIGIN
Query Match 89.5%; Score 17; DB 6; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 GGGTCTGCAGCGGATGCT 19
|||||
Db 1 GGGTCTGCAGCGGATGCT 19
RESULT 25
AX671182

LOCUS AX671182 19 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 22 from Patent WO03004511.
ACCESSION AX671182
VERSION AX671182.1 GI:29329638
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Renzi, P., Allam, M. and Allakhverdi, Z.
TITLE Methods for increasing in vivo efficacy of oligonucleotides and
inhibiting inflammation in mammals
JOURNAL Patent: WO 03004511-A 22 16-JAN-2003;
Topigen Pharmaceuticals Inc (CA)
FEATURES
source location/Qualifiers
1. 19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sequence is completely synthesized"
modified_base 9 /mod_base=1
modified_base 15 /mod_base=1
BASE COUNT 0 a 3 c 10 g 4 t 2 others
ORIGIN
Query Match 89.5%; Score 17; DB 6; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 GGGTCTGCAGCGGATGCT 19
|||||
Db 1 GGGTCTGCAGCGGATGCT 19
RESULT 26
AE004803 10225 bp DNA linear BCT 19-FEB-2003
LOCUS
DEFINITION Pseudomonas aeruginosa PA01, section 364 of 529 of the complete
genome.
ACCESSION AE004803 AE004091
VERSION AE004803.1 GI:9950035
KEYWORDS
SOURCE Pseudomonas aeruginosa PA01
ORGANISM Pseudomonas aeruginosa PA01
REFERENCE 1 (bases 1 to 10225)
AUTHORS Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrenner, P.,
Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J.,
Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E.,
Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N.,
Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H.,
Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Sater, M.H.,
Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen
JOURNAL Nature 406 (6799), 959-964 (2000)
MEDLINE 20437337
PUBMED 10984043
REFERENCE 2 (bases 1 to 10225)
AUTHORS Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrenner, P.,
Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J.,
Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E.,
Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N.,
Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H.,
Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Sater, M.H.,
Hancock, R.E.W., Lory, S. and Olson, M.V.
Direct Submission
TITLE Submitted (16-MAY-2000) Department of Medicine and Genetics,
JOURNAL University of Washington Genome Center, University Of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 10225)

/product="hypothetical protein"
/protein_id="AAG07250.1"
/db_xref="GI:9950041"
/translation="MIEADYLVIGAGIAGASTGYWLSAHGRVVVLEREAPQGYHSTGR
SAHVTAVAGTPOVRAALTAASRAFDNPPAGFCHEPLSPRENVVDFSDPEELARQ
YESGKALVPQMRLLDAQACSIYVLRDKVFGATYDPTGADIDTDLHOGYLRGIR
NOGQVLCNHEALEIRVDGAWVRCDSYRAVLVNAAGMCAIAGLAGVAPLGLQ
PKRRSAFIFAPPPIIDCHDMPMLVSLDESFLKPDAGMLGSPANADPVEAHVQPEO
LDIATGMVLIIEATTLTIRREPHWAGLRSFVADGDLVAGYANAAGFFWVAAGGCG
IOTSAMGEASAAIRHQPLPAHLREHGLDEAMLSPRRLSP"
8098.8730
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8098.8730
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/locus_tag="PA3864"
/note="Protein name confidence: Class 4 (homologs of
previously reported genes of unknown function, or no
similarity to any previously reported sequences)"
/codon_start=1
/transl_table=11

Query Match 89.5%; Score 17; DB 1; Length 10225;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GGCTGCAGCGGATGG 18
Db 8970 GGCTGCAGCGGATGG 8986

RESULT 27
AX066133 436 bp DNA linear PAT 24-JAN-2001
LOCUS Sequence 37 from Patent WO0100804.
DEFINITION AX066133
ACCESSION AX066133.1 GI:12543845
VERSION
KEYWORDS
SOURCE
ORGANISM
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE
1
Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O., Habehauer, G.,
Lee, H.S. and Kim, H.U.
TITLE
corynebacterium glutamicum genes encoding stress, resistance and
tolerance proteins
JOURNAL
Patent: WO 0100804-A 37 04-JAN-2001;
BASF AKTIENGESSELLSCHAFT (DE)
FEATURES
location/Qualifiers
Source
1.436
/organism="Corynebacterium glutamicum"
/mol_type="genomic DNA"
/db_xref="taxon:1718"
101.>436
/note="FRXA02282"
/codon_start=1
/transl_table=11
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/db_xref="GI:12543846"
/translation="MOESSSRDNPQVDIGVVDLLSRHYSGRVYVREILQNAVDACT
ARSEQEGEGYEPSIRIRPVTYKDRATFSLVDNGTGLTAQEARILLATVGRTSKRDEFL
QREGRLGQFG"
BASE COUNT 81 a 102 c 138 g 115 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 6; Length 436;
Best Local Similarity 94.4%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GGCTGCAGCGGATGG 19
Db 401 GGCTGCAGCGGATGG 418

RESULT 28
AB02081540/c 778 bp DNA linear PRI 14-APR-2000
LOCUS AB02081540
DEFINITION Homo sapiens gene for DMBT1, exon 40, complete cds.
ACCESSION AB020851
VERSION AB020851.1 GI:4996276
KEYWORDS
SEGMENT
SOURCE
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Takeshita, H., Sato, M., Shiwa, H.O., Senba, S., Sakurada, A.,
Hoshi, M., Hayashi, Y., Tagawa, Y., Ayabe, H. and Horii, A.
TITLE
Expression of the DMBT1 gene is frequently suppressed in human lung
cancer
JOURNAL
Jpn. J. Cancer Res. 90 (9), 903-908 (1999)
MEDLINE
20017478
PUBMED
10551316
REFERENCE
2 (bases 1 to 778)
AUTHORS
Horii, A.
TITLE
Direct Submission
JOURNAL
Submitted (06-DEC-1998) Akira Horii, Tohoku University School of
Medicine, Department of Molecular Pathology; 2-1 Seiryomachi,
Aoba-ku, Sendai, Miyagi 980-8575, Japan
(E-mail: horii@mail.cc.tohoku.ac.jp, Tel: 81-22-717-8042,
Fax: 81-22-717-8047)
FEATURES
Location/Qualifiers
Source
1.778
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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AB020817.1:89..136,AB020818.1:74..397,AB020819.1:84..113,
AB020820.1:79..120,AB020821.1:90..413,AB020822.1:80..109,
AB020823.1:85..117,AB020824.1:85..408,AB020825.1:84..113,
AB020826.1:77..115,AB020827.1:83..406,AB020828.1:81..110,
AB020829.1:78..110,AB020830.1:84..407,AB020831.1:83..112,
AB020832.1:81..113,AB020833.1:79..402,AB020834.1:84..113,
AB020835.1:73..105,AB020836.1:81..404,AB020837.1:78..107,
AB020838.1:78..116,AB020839.1:92..415,AB020840.1:77..103,
AB020841.1:82..114,AB020842.1:79..232,AB020843.1:88..290,
AB020844.1:83..403,AB020845.1:88..108,AB020846.1:84..113,
AB020847.1:80..230,AB020848.1:81..289,AB020849.1:84..268,
AB020850.1:86..495,74..350)
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join(AB020812.1:179..239,AB020813.1:78..107,
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AB020817.1:89..136,AB020818.1:74..397,AB020819.1:84..113,
AB020820.1:79..120,AB020821.1:90..413,AB020822.1:80..109,
AB020823.1:85..117,AB020824.1:85..408,AB020825.1:84..113,
AB020826.1:77..115,AB020827.1:83..406,AB020828.1:81..110,
AB020829.1:78..110,AB020830.1:84..407,AB020831.1:83..112,
AB020832.1:81..113,AB020833.1:79..402,AB020834.1:84..113,
AB020835.1:73..105,AB020836.1:81..404,AB020837.1:78..107,
AB020838.1:78..116,AB020839.1:92..415,AB020840.1:77..103,
AB020841.1:82..114,AB020842.1:79..232,AB020843.1:88..290,
AB020844.1:83..403,AB020845.1:88..108,AB020846.1:84..113,
AB020847.1:80..230,AB020848.1:81..289,AB020849.1:84..268,
AB020850.1:86..495,74..350)
/gene="DMBT1"
/codon_start=1
/product="DMBT1"
/protein_id="BAA78577.1"
/db_xref="GI:4996278"
/translation="MGISTVILEMCLMGQVLSTGWIPTTDTYASLIPSEVPLDTTV
AEGSPFSELTLESTVAEGSPISLESTLESTVAEGSLIPSELTLESTVAEGSDGLAL
RLVNGDGCQGRVEILYRGSGTVCDSWDNTDANVVRQLGCGWAMAPGNAMFGQG
SGPIALDVRCSGHESYLSCPHNGWLSHNGCHGEDAGVICSAAQPGSTLRPESWPR
ISPPVTEGSESSIALRLVNGDRCGRVEVLVYRGSGTVCDDYWDNTDANVVRQLG
CGWAMAPGNAMFGQSGSPILVDVRCGHESYLSCPHNGWLTTHNGHSEDAGVICS

APQSRPTSPDTWPTSHASTAGSSSLALRLVNGDRCQGRVEVLYRGSWGTVCDDSM
 DTSADVNCRLGCGWATSAPGNARFGQSGPIVLDDVRCSGEYLSLWSCPHNGWLSH
 NCOHSEDAGVICSAAHSWSTPSPTLPTITLPASTVGSSESLALRLVNGDRCQGRVE
 VLYQSGWGTVCDDSWDTNDANVCRQLGCGWAMAPGNARFGQSGPIVLDDVRCSGH
 ESYLWSCPHNGWLSHNCGHSEDAGVICSASQSRPTSPDTWPTSHASTAGSESLALR
 LVNGDRCQGRVEVLYRGSWGTVCDDYNDANVCRQLGCGWAMAPGNARFGQSG
 GPIVLDDVRCSGHESYLSWSCPHNGWLSHNCGHEDAGVICSASQSRPTSPDTWPTSH
 ASTAGSESLALRLVNGDRCQGRVEVLYRGSWGTVCDDYNDANVCRQLGCGWA
 TSAPGNARFGQSGPIVLDDVRCSGHESYLSWSCPHNGWLSHNCGHEDAGVICSASQ
 OPTSPDTWPTSHASTAGSESLALRLVNGDRCQGRVEVLYQSGWGTVCDDYND
 ANVCRQLGCGWAMAPGNARFGQSGPIVLDDVRCSGHESYLSWSCPHNGWLSHNCGH
 HEDAGVICSASQSRPTSPDTWPTSHASTAGSESLALRLVNGDRCQGRVEVLYR
 GSWGTVCDDSWDTNDANVCRQLGCGWAMAPGNARFGQSGPIVLDDVRCSGHESYL
 WSCPHNGWLSHNCGHEDAGVICSATQINSTTDMWHPTTTTARPPSSNCGFLPYAS
 GTFSSPSYPAYYPNNACVWEIENSGYRINLGFSLNLEAHNCSFDYVEIPDGLN
 SSLLGKICNDTRQIFTSYNNMTIHFSDISFNTGFLAWNSFPDATTALRLVNLNLS
 SYGLCAGRVEIYHGTWGTVCDDSWTIQAEVVCRLGCGRAVALGNAYFGSGSGPI
 TLDDVECSGTESTLMQCRNGWFSHNCNREDAGVICSGNHSTPAFLNITRPNTDY
 SCGGFLSQPSGDSPPFYPGNYPNNACVWDIEVQNNYRTVIRPDVQLEGCCNYDYI
 EVFDGPYRSSPLIARVCDGARGSTSSSNFMSIRFISDHSITTRGFRAEYSSPNDIS
 TNLICLPNHMQASVRSYLSQSLGASADLVISTWNGYECRPOITPNLVIPTIYSGC
 GTFKQADNDTIDVSNFLTAASGGLIKRTDLRIHVSRCMLQNTWDTMYIANDTIHV
 ANNTIQVEEVQNGFDVNIISFTSSSFLYPTSRPYVDLNDLYVQAEIILHSDAVLT
 LFVDTCVASPYSNDFSTLTYDLIRSGCVRDDTYGPYSSPLRIARFRFAFHFLNRP
 SVYLCKMVCRAYPDSSRCYRGCVLRKRDVGSYQEKVDVLGPILQLOTPPRREEEP
 R"

intron
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 /number=39
 74. .>778
 /product="DMBT1"

exon
 /number=40

BASE COUNT 160 a 216 c 205 g 197 t
 ORIGIN

Query Match 86.3%; Score 16.4; DB 9; Length 778;
 Best Local Similarity 94.4%; Pred. No. 2.3e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTCTGACGGGATGG 18
 |||||
 Db 321 GGCTCTGACGTGGATGG 304

RESULT 29
 AB006797/c 1468 bp DNA linear BCT 01-MAY-1999
 LOCUS
 DEFINITION Pseudomonas aeruginosa oprQ gene for OprQ, complete cds.
 ACCESSION AB006797
 VERSION AB006797.1 GI:2425171
 KEYWORDS OprQ.
 SOURCE Pseudomonas aeruginosa
 ORGANISM Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 REFERENCE 1 (sites)
 AUTHORS Okamoto,K., Gotoh,N., Tsujimoto,H., Yamada,H., Yoshihara,E.,
 Nakae,T. and Nishino,T.
 TITLE Molecular cloning and characterization of the oprQ gene coding for
 outer membrane protein OprQ of Pseudomonas aeruginosa
 JOURNAL Microbiol. Immunol. 43 (3), 297-301 (1999)
 MEDLINE 99268523
 PUBMED 10338201
 REFERENCE 2 (bases 1 to 1468)
 AUTHORS Tsujimoto,H.
 TITLE Direct Submission
 JOURNAL Submitted (22-AUG-1997) Hideoto Tsujimoto, Kyoto Pharmaceutical
 University, Laboratory of Microbiology; Misaaki Nakauchi-chou 5,
 Yamashina, Kyoto, Kyoto 607, Japan
 (E-mail:htsujimo@mb.kyoto-phu.ac.jp, Tel:+81-75-595-4642,
 Fax:+81-75-583-2230)
 FEATURES
 Location/Qualifiers
 1. 1468

/organism="Pseudomonas aeruginosa"
 /mol_type="genomic DNA"
 /strain="PAO1"
 /db_xref="taxon:287"
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 -10_signal 117. .122
 RBS 148. .151
 gene 160. .1437
 CDS /gene="oprQ"
 160. .1437
 /gene="oprQ"
 /codon_start=1
 /transl_table=11
 /product="OprQ"
 /protein_id="BAA22267.1"
 /db_xref="GI:2425172"
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 ISRDYKHGRQDKAEWQAAITFTSGFTQTVGVDAFGLYAVRLDGKSGAAGI
 DFFKQDGSAAADLSKGAIVKFRISNTVLKGDQMSLPVLSYDNRILPESYSGT
 LITSEIEGLEINAGRFTAERKSAEGRDGGILKSINVEGKYAFTDHFNASLIASDV
 EDVLKKQYINLNYTIPLOADQSLNFDENGYRTKLSDFADQNFNDRDNKIKWSLAAY
 TIDGTFMIAHORNTGTGYNGWYQNAIGIGDGTITWLANSYWSDFNAEDERSWQV
 SYALDFAKYGVPLTRYVAAYRGDNIKTAETSNKEREIFNQVQVVSQPAKDLTLR
 LRSSFRLVRSNDARSYNDDGNETIRAFVEYPFVSF"

mat_peptide

BASE COUNT 332 a 485 c 421 g 230 t
 ORIGIN

Query Match 86.3%; Score 16.4; DB 1; Length 1468;
 Best Local Similarity 94.4%; Pred. No. 2.2e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCTCTGACGGGATGGT 19
 |||||
 Db 870 GGCTCTGACGGGATGGT 853

RESULT 30
 AX120193 1824 bp DNA linear PAT 11-MAY-2001
 LOCUS
 DEFINITION Sequence 109 from Patent EP1108790.
 ACCESSION AX120193
 VERSION AX120193.1 GI:14036908
 KEYWORDS
 SOURCE Corynebacterium glutamicum
 ORGANISM Corynebacterium glutamicum
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 REFERENCE 1
 AUTHORS Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
 Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
 TITLE Novel polynucleotides
 JOURNAL Patent: EP 1108790-A 109 20-JUN-2001;
 KIOWA HAKKO KOGYO CO., LTD. (JP)
 FEATURES
 Location/Qualifiers
 1. 1824
 /organism="Corynebacterium glutamicum"
 /mol_type="genomic DNA"
 /db_xref="taxon:1718"

BASE COUNT 375 a 466 c 538 g 445 t
 ORIGIN

Query Match 86.3%; Score 16.4; DB 6; Length 1824;
 Best Local Similarity 94.4%; Pred. No. 2.1e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCTCTGACGGGATGGT 19
 |||||
 Db 301 GGCTCTGACGGGATGGT 318

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RESULT 31
BD162310
LOCUS      BD162310          1824 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Novel polynucleotide.
ACCESSION  BD162310
VERSION     BD162310.1 GI:27868067
KEYWORDS    JP 2002191370-A/109.
SOURCE      unidentified
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 1824)
AUTHORS     Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
            Yokoi,H., Tateishi,N., Senoo,A., Ikeda,M. and Ozaki,A.
TITLE       Novel polynucleotide
JOURNAL     Patent: JP 2002191370-A 109 09-JUL-2002;
            KYOMA HAKKO KOGYO CO LTD
COMMENT     OS   Corynebacterium glutamicum
            PN   JP 2002191370-A/109
            PD   09-JUL-2002
            PF   15-DEC-2000 JP 2000405096
            PI   SATOSHI NAKAGAWA,HIROSHI MIZOGUCHI,SEIKO ANDO,MIKIO HAYASHI,
            PI   KEIKO OCHIAI,
            PI   HARUHIKO YOKOI,NAOKO TATEISHI,AKIHIRO SENOO,MASATO IKEDA,AKIO
            PI   OZAKI
            PC   C12N15/09,C12N15/09,C07K14/34,C07K16/12,C07K16/40,C12M1/00,PC
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12N9/02,C12P7/40,C12P13/
            PC   04,C12P13/08,
            PC   C12P19/00,C12P19/34,C12P21/02,C12Q1/37,C12Q1/68,G01N33/53,PC
            G01N33/566,
            PC   G01N33/569,G01N33/68,G01N37/00//C12P21/08,(C12N1/21,C12R1:15),
            PC   (C12N1/21,C12R1:13),(C12N1/21,C12R1:01),(C12P13/08,C12R1:15),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00
            CC   Novel polynucleotide
            FH   Key
            FT   source
            FT   1.1824
            FT   location/Qualifiers
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            FT   /organism='Corynebacterium glutamicum'.
            FT   1.1824
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            FT   /db_xref="taxon:32644"

BASE COUNT      375 a      466 c      538 g      445 t

ORIGIN
Query Match      86.3%; Score 16.4; DB 6; Length 1824;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGTCTGACGGGATGCT 19
        |||||
        301 GGTCTGACGGGAGGT 318

Db
301 GGTCTGACGGGAGGT 318

RESULT 32
AX066131
LOCUS      AX066131          1947 bp      DNA      linear      PAT 24-JAN-2001
DEFINITION Sequence 35 from Patent WO0100804.
ACCESSION  AX066131
VERSION     AX066131.1 GI:12543843
KEYWORDS
SOURCE      Corynebacterium glutamicum
ORGANISM    Corynebacterium glutamicum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE   1
AUTHORS     Pompejus,M., Kroeger,B., Schroeder,H., Zelder,O., Haberhauer,G.,
            Lee,H.S. and Kim,H.J.
TITLE       corynebacterium glutamicum genes encoding stress, resistance and
            tolerance proteins
JOURNAL     Patent: WO 0100804-A 35 04-JAN-2001;

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FEATURES
SOURCE      BASF AKTIENGESellschaft (DE)
            Location/Qualifiers
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            101.1927
            /note="RXN02280"
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            /transl_table=11
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            /db_xref="GI:12543844"
            /translation="MQESSRDNFQVDLGGVVDLLSRHYSRPRVYRELLQNAVDACT
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            OREGRLGQFGIGLSCFVADETMTVSHAGASAIRMTGADGTNLEIGDDATDVI
            PVGTVHLTPRPDERTLTENS SVTTIASNYGRYLPPIVVGKNTTITSPVFAKDT
            DQQRLYAGBERLGTTPVDVIDLTGPGIEGAVYVPEAQPHMSRHSIYVRMLVSD
            GPSTVLPNMAFFVECEINSTDLPTASREALMDDTAFATREHIGECIKSWLINLMT
            KPHRVREPTAHDALRELQSDADLAETMLGLTLTETSGRISIGEITLITSDVS
            MELPPLQDIEKAKALDAQTESLKDFOIKGATRVFEPADYPAVVIIDSKAQRDRNE
            TOSATTDRAWADILATVDNTLSROTANIPDOGLSALCLNNNSLVKRLASTYDDTAVVS
            RTVRLLYQALLSSKRPLRVKERALLNDLADLVLSLSSDI"

BASE COUNT      399 a      502 c      562 g      484 t

ORIGIN
Query Match      86.3%; Score 16.4; DB 6; Length 1947;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGTCTGACGGGATGCT 19
        |||||
        401 GGTCTGACGGGAGGT 418

Db
401 GGTCTGACGGGAGGT 418

RESULT 33
BC015649/c
LOCUS      BC015649          2097 bp      mRNA      linear      PRI 09-OCT-2001
DEFINITION Homo sapiens, similar to RIKEN cDNA 0610020I02 gene, clone
ACCESSION  MGC:23427 IMAGE:4654320, mRNA, complete cds.
VERSION     BC015649
KEYWORDS    BC015649.1 GI:15990514
SOURCE      MGC.
ORGANISM    Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
            1 (bases 1 to 2097)
            Strausberg,R.
            Direct Submission
            Submitted (04-OCT-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.nci.nih.gov
            Contact: MGC help desk
            Email: gcgabs-remail.nih.gov
            Tissue Procurement: DCTD/DTF
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@hgri.nih.gov
            Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,B., Legaspi,R.,
            Lim,M., Maduro,Q.L., Masello,C., Maserian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Snyder,B., Stantiriop,S., Thomas,P.J.,
            Tongson,E.B., Touchman,J.W., Tsurgon,C., Vogt,J.L., Walker,M.A.,
            Zhang,L.-H. and Green,E.D.

```


Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINt at: <http://image.lnl.gov>
Series: IRAL Plate: 33 Row: 1 Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES Location/Qualifiers

1..2097
/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="Skin, melanoma, amelanotic"
/clone_id="N1H MGC_41"
/lab_host="DH10B-R"
/note="Vector: POTB7"
151..1914
/codon_start=1
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/protein_id="AAH15649.1"
/db_xref="GI:15990515"
/translation="MSQMLHIEIPNGNTVLGCLNEORLLGLYCDVSIIVKGAFAKRAVLAASSLYFRDLFGNSKSAFELPGSVPPACFOQILSPCYTGRLLTMTASEQLVVMYTAGFLQIOHIVERGTDLMFKVSSPHCDSTAVIBDAGSEPOSPCNOLQPAAPAAAPVVSBSVPILPLTRVHEAMELPPAGGLAPKPLETGPRDGAVAAGAAVAGTAPLKLPRVSYGVPSLATLIPGIQMPYQGERSTPGASSLPTTDSPTSANEDEDEDDAYDTHVEEQYQMVIKASGSYAVQEKBPVPLESRCTVLRDLVALPASLISQIGYRCHPKLYSEGDPGEKLELVAGSVYITRGOLMCHLCAGVKHKLRLPLATFPDRNTLANS CGTGRSSTSDPSRKLDSRVLANVLYCQNFAPSKSEMANVTAADMCTNARYRKR WLPKIKSMLPEGVEMRTVMGSAASVPLDPEFPAAQVFEORTYAEARGDAATIVA LRTDAVNVDLSAANPAFDAGEVDGAGSVIQEVAAPELPADGOSPPQPFEGGSGGP SRPOTPAAARPRPGTYAGTL"

BASE COUNT 394 a 740 c 658 g 305 t

Query Match 86.3%; Score 16.4; DB 9; Length 2097;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGTCTGACGGGATGG 18
Db 664 GGGTCAGCAGCGGATGG 647

RESULT 34
MLCPMOA/c 4690 bp DNA linear BCT 15-JUN-2001
LOCUS Methylococcus capsulatus particulate methane monooxygenase subunit
DEFINITION (pmoC1), particulate methane monooxygenase 27 kDa subunit (pmoA),
and particulate methane monooxygenase 45 kDa subunit precursor
(pmoB) genes, complete cds.

ACCESSION L40804
VERSION L40804.2 GI:14456718

KEYWORDS Methylococcus capsulatus
SOURCE Methylococcus capsulatus
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
Methylococcaceae; Methylococcus.

REFERENCE 1 (bases 1 to 4690)
AUTHORS Semrau, J.D., Christoserdov, A., Lebrun, J., Costello, A., Davagnino, J.,
Kenna, E., Holmes, A.J., Finch, R., Murrell, J.C. and Lidstrom, M.E.

TITLE Particulate methane monooxygenase genes in methanotrophs
JOURNAL J. Bacteriol. 177 (11), 3071-3079 (1995)

MEDLINE 95286486
PUBMED 7768803
REFERENCE 2 (bases 1432 to 4689)
AUTHORS Lidstrom, M.E.
TITLE Direct Submission
JOURNAL Submitted (14-MAR-1997) Chemical Engineering, University of
Washington, Seattle, WA 98195, USA

REFERENCE 3 (bases 1 to 4690)
AUTHORS Stolyar, S.E. and Lidstrom, M.E.
TITLE Direct Submission

JOURNAL Submitted (06-JUN-2000) Chemical Engineering, University of
Washington, Seattle, WA 98195, USA
REMARK Sequence updated by submitter
COMMENT On Jun 15, 2001 this sequence version replaced gi:1894817.
FEATURES Location/Qualifiers

SOURCE

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/mol_type="genomic DNA"
/strain="Batch"
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/protein_id="AAB49820.1"
/db_xref="GI:1894818"
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WSAGLDSFAPBEETVMNLFYTEIVLEIVTASILWGLWTKRDLALTPREELRN
FTHLVWLVAVAMAIYWGASVFTBQDGTWQTIVRDFTFPGHIEFYLSPIYIITGF
AAFIYAKTRLPPEFAKGISLPYLVLVGVGFMILPNVGLNEWGHTFWMELFVAPLHYG
FVIFGWLALAVMGTLTQTFFRFAQGGIGGSLCEAVDEGLAK"

gene 2482..3237
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2482..2486
/gene="pmoA"
/note="putative"
2494..3237
/gene="pmoA"
/note="pmoA"
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subunit"
/protein_id="AAB49821.1"
/db_xref="GI:790831"
/translation="MSAAQSAVRSAAEAVOVSRITDMMALFVVFVIVGSYHIHMLT
MGDWDFWSDWKDRLMVTYTPVLTVPFAVQSYLMERYRLPWGATVCVGLLGEWI
NRYFNFMGWTFPFINFVPASLVPGAILDVTMLSGSYLFTAIVGAMGWGLIFPGN
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3334..3337
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RTIHMYDLSMSKEKVKINETYIKGKHFVPEGMPELTVDEPVAFLNVGMPGVFIKKE
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GSMSEFRNPVTTLTGQTVDLNENGTTFMHAFWFAIGVAMIGWSRPIPIRLLM
VDAGRADELVSATDRKVMGFLAATLILVVMAMSSANSKYPTITPLQAGTWGKMPLE
LPAPTVSVKVEDATYRVPGRAMRMKLTITNGNSPIRIGEFYASVRFSDSDVYKDTT
GYPEDLAEDELVSVDNSPLAGETRTVDVTASDAAMEVYRLSDIITYDPSRFAGLLP
FPDATGNRQVVQIDAPLIPSTF"

sig_peptide 3344..3442
mat_peptide 3443..4585

BASE COUNT 900 a 1400 c 1438 g 952 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 1; Length 4690;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCTGCACCGGATGT 19
Db 4141 GGCCTGCACGGATGT 4124

RESULT 35
A90822/c
LOCUS A90822 5802 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1 from Patent WO9830687.
ACCESSION A90822
VERSION A90822.1 GI:6739232
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 5802)
AUTHORS Poustka, A. and Mollenhauer, J.
TITLE PROTEIN CONTAINING AN SRCR DOMAIN
JOURNAL Patent: WO 9830687-A 1 16-JUL-1998;
DEUTSCHES KREBSFORSCH (DE); POUSTKA ANNEMARIE (DE)

FEATURES
source 1..5802
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
107..5464
/note="unnamed protein product"
/codon_start=1
/protein_id="CAB69392.1"
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AEGSPFSESTLESTAEGSPISLESTLESTAEGSLIPSESTLESTAEGSDGLAL
RLVNGDRCQGRVEILYRGSGWTCDDSDWDNDANVCRQLGCGWASAPGNAMFGOG
SGPIALDVRCSGHESYLWSCPHNGWLSHNCGHEDAGVCSAQPSTLRPSWVR
ISPPVTEGSESSLALRLVNGDRCGRVEVLYRGSGWTCDDWDNDANVCRQLG
CGWASAPGNAMFGOGSGPIVLDVRCSGHESYLWSCPHNGWLSHNCGHEDAGVCS
APQSRPTSPDPTWPTSHASTAGSESSLALRLVNGDRCGRVEVLYRGSGWTCDDSW
DTSADVCRQLGCGWATAPGNARFGOGSGPIVLDVRCSGHESYLWSCPHNGWLSH
NCQSEDAGVCSAHSWSTSPDPTLPTITLPAVSGSESSLALRLVNGDRCGRVE
VLYRGSGWTCDDSDWDNDANVCRQLGCGWASAPGNARFGOGSGPIVLDVRCSGH
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LVNGDRCGRVEVLYRGSGWTCDDWDNDANVCRQLGCGWASAPGNARFGOGS
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TSAPGNARFGOGSGPIVLDVRCSGHESYLWSCPHNGWLSHNCGHEDAGVCSASQ
OPTSPDPTWPTSHASTAGSESSLALRLVNGDRCGRVEVLYRGSGWTCDDWDND
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WSCPHKGLTHNCGHEDAGVCSATQINSTTDMWHTTTTARPSNCGGFLFYAS
GTSSPSYPAYYNNACWKEVNSGYRINLGFSLKLEAHNCSFDYVBIPTGSLN
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SYGLCAGRVEIYHGTCGTCWTCIOAEVYCRQLGCGWASAPGNARFGOGSGPI
TLDDVECSGTESTLMQCRNKGFSHNCNHRDAGVCSGNHSTPAPFLNTRPNTDY
SCGFLSOPSGDFSSPFYPGNYPNNACWMDLEVQNNYRVTVI FRDVLGEGCNVDYI
EVFDGPTRRSSPLARVCDGARGSTSSNFMISIRFISDHSITRRGFAEYSSPSNDS
TNLLCLPNHMOASVRSYLOSIGFSASDLVISTWNGYECRPOITPNLVIPTIYSGC
GTFKQADNDITDYSNFLTAAVSGGIIKRTDRIHVSCHRMQNTWDTMYIANDTITHV
ANNTIOVEEVOYGNFDVNIISFYTSSSFLYPTSRPYVDLQDLVQAEILHSDAVLT
LFVDTCVASPYSDNTSLTYDLIRSGCVRDDTYGPYSSPSLRIARFRFRAHFHLNRP
SVYLRCKMVCRAVYDPSSRCYRCVLRSKRDVGSYQEKVDVVLGPIQLQTPRREEBP
R"

BASE COUNT 1253 a 1614 c 1576 g 1359 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 6; Length 5802;
Best Local Similarity 94.4%; Pred. No. 1.8e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGCACCGGATGG 18
Db 5435 GGGTCTGCACGCTGGATGG 5418

RESULT 36
AR193170/c
LOCUS AR193170 5802 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4 from patent US 6346606.
ACCESSION AR193170
VERSION AR193170.1 GI:20239135
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 5802)
AUTHORS Mollenhauer, J. and Poustka, A.
TITLE Protein containing a scavenger receptor cysteine rich domain
JOURNAL Patent: US 6346606-A 4 12-FEB-2002;
FEATURES location/Qualifiers
source 1..5802
/organism="unknown"

BASE COUNT 1253 a 1614 c 1576 g 1359 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 6; Length 5802;
Best Local Similarity 94.4%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGCACCGGATGG 18
Db 5435 GGGTCTGCACGCTGGATGG 5418

RESULT 37
BD064963/c
LOCUS BD064963 5802 bp DNA linear PAT 27-AUG-2002
DEFINITION Protein containing an SRCR domain.
ACCESSION BD064963
VERSION BD064963.1 GI:22610566
KEYWORDS JP 2001509667-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 5802)
AUTHORS Mollenhauer, J. and Poustka, A.
TITLE Protein containing an SRCR domain
JOURNAL Patent: JP 2001509667-A 1 24-JUL-2001;
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OFFENTLICHEN RECHTS
COMMENT OS Homo sapiens (human)
PN JP 2001509667-A/1
PD 24-JUL-2001
PF 09-JAN-1998 JP 1998530469
PR 09-JAN-1997 DE 197 00 519.5, 18-JUL-1997 DE 197 30 997.6 PI
JAN MOLLENHAUER, ANNEMARIE POUSTKA
PC C12N15/12, C12N15/70, C12N1/21, C12Q1/68, C07K14/47, C07K16/18, PC
A61K8/17,
PC A61K48/00, G01N33/50
CC Protein containing an SRCR domain
FH Key location/Qualifiers
FT CDS (107)..(5461).

FEATURES
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
location/Qualifiers
1..5802

BASE COUNT 1253 a 1614 c 1576 g 1359 t
ORIGIN

Query Match 86.3%; Score 16.4; DB 6; Length 5802;

Best Local Similarity 94.4%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGTCTGCAGCGGATGG 18
|||||
Db 5435 GGGTCTGCAGCTGATGG 5418

RESULT 38
HSDMBT1/c 5802 bp mRNA linear PRI 27-NOV-2000
LOCUS HSDMBT1
DEFINITION Homo sapiens mRNA for DMBT1 6 kb transcript variant 1 (DMBT1 gene).
ACCESSION AJ000342
VERSION AJ000342.1 GI:2398620
KEYWORDS alternative splicing; deleted in malignant brain tumors 1; DMBT1 gene; DMBT1/6kb.1 protein; tumor suppressor; tumour suppressor.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Mollenhauer J., Wiemann S., Scheurle W., Korn B., Hayashi Y.,
AUTHORS Wilgenbus K.K., von Deimling A. and Poustka A.
TITLE DMBT1, a new member of the SRCR superfamily, on chromosome
JOURNAL 10q25.3-26.1 is deleted in malignant brain tumours
MEDLINE Nat. Genet. 17 (1), 32-39 (1997)
PUBMED 97434209 9288095

REFERENCE 2 (bases 1 to 5802)
AUTHORS Mollenhauer J.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-1997) Mollenhauer J., Molecular Genome Analysis,
German Cancer Research Center, Im Neuenheimer Feld 280, Heidelberg,
D-69120, GERMANY

FEATURES
source Location/Qualifiers

1..5802
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Best Local Similarity 94.4%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 39
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LOCUS MCU94337/c
DEFINITION Methylococcus capsulatus formylmethanofuran dehydrogenase subunit
A-like protein gene, partial cds; and formylmethanofuran
tetrahydromethanopterin formyltransferase-like protein,
formylmethanofuran dehydrogenase-like protein, methane
monooxygenase subunit C2 (pmoC2), methane monooxygenase subunit A2
(pmoA2), and methane monooxygenase subunit B2 (pmoB2) genes,
complete cds.
U94337 AF273026
U94337.2 GI:13559968

ACCESSION U94337 AF273026
VERSION U94337.2 GI:13559968
KEYWORDS Methylococcus capsulatus
SOURCE Methylococcus capsulatus
ORGANISM Methylococcus capsulatus
Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
Methylococcaceae; Methylococcus.
1 (bases 1 to 7080)
Stolyar, S., Costello, A.M., Peoples, T.L. and Lidstrom, M.E.
Role of multiple gene copies in particulate methane monooxygenase
activity in the methane-oxidizing bacterium Methylococcus
capsulatus Bath
Microbiology 145 (Pt 5), 1235-1244 (1999)

REFERENCE 1 (bases 1 to 7080)
AUTHORS Stolyar, S., Costello, A.M., Peoples, T.L. and Lidstrom, M.E.
TITLE Role of multiple gene copies in particulate methane monooxygenase
activity in the methane-oxidizing bacterium Methylococcus
capsulatus Bath
Microbiology 145 (Pt 5), 1235-1244 (1999)

JOURNAL MEDLINE 10376840
PUBMED 99303333
REFERENCE 2 (bases 1 to 7080)
AUTHORS Stolyar, S., Peoples, T.L., Costello, A.M. and Lidstrom, M.E.
TITLE Direct Submission
JOURNAL Submitted (05-MAR-1997) Chemical Engineering, University of
Washington, Seattle, WA 98195, USA

REFERENCE 3 (bases 1 to 7080)
AUTHORS Stolyar, S., Franke, M. and Lidstrom, M.E.
TITLE Expression of individual copies of Methylococcus capsulatus bath
particulate methane monooxygenase genes
J. Bacteriol. 183 (5), 1810-1812 (2001)
JOURNAL MEDLINE 21101880
PUBMED 11160118
REFERENCE 4 (bases 1 to 7080)
AUTHORS Stolyar, S., Franke, M. and Lidstrom, M.E.
TITLE Direct Submission

JOURNAL

Submitted (06-APR-2001) Chemical Engineering, University of Washington, Seattle, WA 98195, USA
Sequence update by submitter
On Apr 6, 2001 this sequence version replaced gi:1913910.
location/Qualifiers

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BASE COUNT

ORIGIN 1341 a 2138 c 2220 g 1381 t

Query Match

Best Local Similarity 94.4%; Pred. No. 1.8e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

2 GGTCTGCAGCGGATGCT 19

Db 6346 GGCTTGACAGCGGATGCT 6329

RESULT 40

HSA243224/c

LOCUS

DEFINITION

Homo sapiens mRNA for DMBT1 protein 8kb transcript variant 1 (DMBT1/8kb.1).

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCES

AUTHORS

TITLE

JOURNAL

MEDLINE

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REFERENCES

AUTHORS

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Best Local Similarity 94.4%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 GGGTCTGCAGCGGATGG 18

Db 7289 GGGTCTGCAGCTGATGG 7272
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Job time : 748 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2004, 15:53:18 ; Search time 123.5 seconds
(without alignments)
415.298 Million cell updates/sec

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Perfect score: 19
Sequence: 1 gggctcgcagcgagatgct 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	19	100.0	19	25	ABX12700
5	19	100.0	619	23	AA570201
6	19	100.0	3394	25	AAD51325
7	19	100.0	3439	25	ABX63546
8	19	100.0	3475	13	AAQ21453

C	9	19	100.0	21968	25	AAD51326	Human receptor gen
C	10	19	100.0	86574	24	ABK83560	Human cDNA differe
C	11	18	94.7	19	21	AAZ56194	Oligonucleotide 10
C	12	18	94.7	19	21	AAZ56195	Oligonucleotide 10
C	13	18	94.7	19	25	ABX12689	Human IL-3/IL-5/GM
C	14	18	94.7	19	25	ABX12690	Human IL-3/IL-5/GM
C	15	17	89.5	19	21	AAZ56199	Oligonucleotide 10
C	16	17	89.5	19	25	ABX12694	Human IL-3/IL-5/GM
C	17	17	89.5	19	25	ABX12701	Human IL-3/IL-5/GM
C	18	17	89.5	19	25	ABX12702	Human IL-3/IL-5/GM
C	19	16.4	86.3	256	22	AAK63218	Human immune/haema
C	20	16.4	86.3	436	22	AAF71002	C. glutamicum SRT
C	21	16.4	86.3	535	22	AAK84431	Human immune/haema
C	22	16.4	86.3	536	22	AAK84430	Human immune/haema
C	23	16.4	86.3	825	23	AA567706	DNA encoding novel
C	24	16.4	86.3	825	23	AA583466	DNA encoding novel
C	25	16.4	86.3	1095	21	AAA72267	Drosophila odorant
C	26	16.4	86.3	1194	21	AAA94826	Drosophila melanog
C	27	16.4	86.3	1197	23	ABL06359	Drosophila melanog
C	28	16.4	86.3	1320	24	ABQ90060	M. capsulatus gene
C	29	16.4	86.3	1443	24	ABQ90381	M. capsulatus gene
C	30	16.4	86.3	1537	21	AACT9967	Human secreted pro
C	31	16.4	86.3	1824	22	AAH65074	C glutamicum codin
C	32	16.4	86.3	1947	22	AAF71001	C glutamicum SRT
C	33	16.4	86.3	3309	23	ABL06358	Drosophila melanog
C	34	16.4	86.3	5802	19	AAV49652	Human SRCR protein
C	35	16.4	86.3	8045	22	AA533414	DNA encoding human
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C	37	16.4	86.3	21719	23	AA559568	Protonibacterium
C	38	16.4	86.3	28720	19	AAV49655	Human SC3 DNA. Ho
C	39	16.4	86.3	349980	22	AAH64966	C glutamicum codin
C	40	16	84.2	19	21	AAZ56196	Oligonucleotide 11
C	41	16	84.2	19	25	ABX12691	Human IL-3/IL-5/GM
C	42	16	84.2	7217	23	ABL07535	Drosophila melanog
C	43	16	84.2	10131	23	ABL07534	Drosophila melanog
C	44	15.8	83.2	305	21	AAA44554	Human secreted exp
C	45	15.8	83.2	624	23	AA570202	DNA encoding novel

ALIGNMENTS

AAZ56193	standard; DNA; 19 BP.
AAZ56193	
28-MAR-2000	(first entry)
XX	Oligonucleotide 107A for IL-3/IL-5/GM-CSF receptor expression inhibition.
DE	interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
XX	asthma; allergy; cancer; receptor expression inhibitor; cytokine;
KW	inflammation; hyper eosinophilia; eosinophil proliferation;
KW	granulocyte macrophage colony stimulating factor; GM-CSF; ss.
XX	
OS	Homo sapiens.
XX	
XX	WO9966037-A2.
PN	
XX	
PD	23-DEC-1999.
XX	
PF	17-JUN-1999; 99WO-CA00572.
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PR	17-JUN-1998; 98CA-2235420.
XX	
PA	(REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
XX	
PI	Renzi P;
XX	
DR	WPI; 2000-097743/08.

PT Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT macrophage colony stimulating factor receptors, used for treating or
PT preventing asthma, allergies, hypereosinophilia, inflammation or cancer
XX
PS Claim 5; Page 23; 72pp; English.
XX
CC This is an antisense oligonucleotide directed against the common beta
CC subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
CC receptor and the granulocyte macrophage colony stimulating factor
CC (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC involved in eosinophil proliferation and survival, they are increased in
CC asthma and atopic diseases, and are also involved in the indefinite
CC proliferation of certain neoplastic diseases. The invention relates to
CC antisense oligonucleotides directed against a nucleic acid sequence
CC encoding either a chemokine receptor (CCR3), a common subunit of
CC interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC oligonucleotides can be used in the treatment or prevention of asthma,
CC allergy, hypereosinophilia, general inflammation or cancer.
XX
SQ Sequence 19 BP; 2 A; 3 C; 10 G; 4 T; 0 other;
Query Match 100.0%; Score 19; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTCGACGGGATGCT 19
1 |||||
Db 1 GGGTCGACGGGATGCT 19
RESULT 2
ABX12688
ID ABX12688 standard; DNA; 19 BP.
XX
AC ABX12688;
XX
DT 10-MAY-2003 (first entry)
XX
DE Human IL-3/IL-5/GM-CSF receptor DNA, antisense oligonucleotide #1.
XX
KW Human; inflammation; 2',6'-diaminopurine; DAP; antisense therapy;
KW DAP-modified oligonucleotide; pulmonary disease; respiratory disease;
KW neurological disease; cardiovascular disease; rheumatological disease;
KW digestive disease; cutaneous disease; ophthalmological disease;
KW urinary system disease; pathogen infection; genetic disease; cancer;
KW airway; nose; pulmonary fibrosis; adult respiratory distress syndrome;
KW cystic fibrosis; chronic obstructive lung disease; chronic bronchitis;
KW eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis;
KW hypereosinophilia; cardiant; ophthalmological; cyostatic;
KW antiasthmatic; antiallergic; antiinflammatory; immunosuppressive;
KW atopic disease; neoplastic cell proliferation; antisense; IL-3; IL-5;
KW interleukin-3 receptor; interleukin-5 receptor; GM-CSF; ss.
XX
OS Homo sapiens.
XX
PN WO2003004511-A2.
XX
PD 16-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-CA01046.
XX
PR 06-JUL-2001; 2001US-303071P.
XX
PA (TOP1-) TOPIGEN PHARM INC.
XX
PI Renzi P, Allam M, Allakherdi Z;
XX
PF WPI; 2003-247944/24.
XX
PT Increasing in vivo efficacy of a nucleic acid molecule that is

PT administered to a mammal for inhibiting inflammation in mammals,
PT involves incorporating into the nucleic acid molecule at least one
PT nucleotide substitute -
XX
PS Claim 28; Page 11; 63pp; English.
XX
CC The present invention relates to a method for increasing the in vivo
CC efficacy of oligonucleotides and inhibiting inflammation. The
CC oligonucleotides comprise at least one nucleotide substitute of
CC 2',6'-diaminopurine (DAP) and/or its analogue. The DAP nucleotide
CC substitutions are useful for increasing in vivo efficacy of a nucleic
CC acid molecule that is administered to a mammal. The DAP-modified
CC oligonucleotides are useful in antisense therapy for treating and/or
CC preventing pulmonary/respiratory diseases, neurological diseases,
CC cardiovascular diseases, rheumatological diseases, digestive diseases,
CC cutaneous diseases, ophthalmological diseases, urinary system diseases,
CC pathogen infections, genetic diseases, general inflammation and
CC cancers. The respiratory system disease is a sickness associated with
CC an inflammation of the lungs, the airways and/or the nose. The
CC respiratory system disease is selected from pulmonary fibrosis, adult
CC respiratory distress syndrome, cystic fibrosis, chronic obstructive
CC lung disease, chronic bronchitis, eosinophilic bronchitis, asthma,
CC allergy, allergic rhinitis, sinusitis and hypereosinophilia. The
CC DAP-modified oligonucleotides are more stable in the body, more
CC effective, and less toxic than standard antisense oligonucleotides.
CC DAP or its analogues are more effective than other substitutes of
CC adenosine. ABX12681-ABX12698 represent antisense oligonucleotides
CC for treating or preventing atopic diseases and neoplastic cell
CC proliferation.
XX
SQ Sequence 19 BP; 2 A; 3 C; 10 G; 4 T; 0 other;
Query Match 100.0%; Score 19; DB 25; Length 19;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTCGACGGGATGCT 19
1 |||||
Db 1 GGGTCGACGGGATGCT 19
RESULT 3
ABX12699/c
ID ABX12699 standard; DNA; 19 BP.
XX
AC ABX12699;
XX
DT 10-MAY-2003 (first entry)
XX
DE Human IL-3/IL-5/GM-CSF receptor DNA, sense oligonucleotide 107S.
XX
KW Human; inflammation; 2',6'-diaminopurine; DAP; antisense therapy;
KW DAP-modified oligonucleotide; pulmonary disease; respiratory disease;
KW neurological disease; cardiovascular disease; rheumatological disease;
KW digestive disease; cutaneous disease; ophthalmological disease;
KW urinary system disease; pathogen infection; genetic disease; cancer;
KW airway; nose; pulmonary fibrosis; adult respiratory distress syndrome;
KW cystic fibrosis; chronic obstructive lung disease; chronic bronchitis;
KW eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis;
KW hypereosinophilia; cardiant; ophthalmological; cyostatic;
KW antiasthmatic; antiallergic; antiinflammatory; immunosuppressive;
KW atopic disease; neoplastic cell proliferation; IL-3; IL-5;
KW interleukin-3 receptor; interleukin-5 receptor; GM-CSF; ss.
XX
OS Homo sapiens.
XX
PN WO2003004511-A2.
XX
PD 16-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-CA01046.
XX
PR 06-JUL-2001; 2001US-303071P.


```
XX
PA (TOP1-) TOPIGEN PHARM INC.
XX
XX Renzi P, Allam M, Allakhverdi Z;
XX
XX WPI; 2003-247944/24.
XX
XX Increasing in vivo efficacy of a nucleic acid molecule that is
XX administered to a mammal for inhibiting inflammation in mammals,
XX involves incorporating into the nucleic acid molecule at least one
XX nucleotide substitute
XX
XX Examples; Page 18; 63pp; English.
XX
XX The present invention relates to a method for increasing the in vivo
XX efficacy of oligonucleotides and inhibiting inflammation. The
XX oligonucleotides comprise at least one nucleotide substitute of
XX 2',6'-diaminopurine (DAP) and/or its analogue. The DAP nucleotide
XX substitutions are useful for increasing in vivo efficacy of a nucleic
XX acid molecule that is administered to a mammal. The DAP-modified
XX oligonucleotides are useful in antisense therapy for treating and/or
XX preventing pulmonary/respiratory diseases, neurological diseases,
XX cardiovascular diseases, rheumatological diseases, digestive diseases,
XX cutaneous diseases, ophthalmological diseases, urinary system diseases,
XX pathogen infections, genetic diseases, general inflammation and
XX cancers. The respiratory system disease is a sickness associated with
XX an inflammation of the lungs, the airways and/or the nose. The
XX respiratory system disease is selected from pulmonary fibrosis, adult
XX respiratory distress syndrome, cystic fibrosis, chronic obstructive
XX lung disease, chronic bronchitis, eosinophilic bronchitis, asthma,
XX allergy, allergic rhinitis, sinusitis and hypereosinophilia. The
XX DAP-modified oligonucleotides are more stable in the body, more
XX effective, and less toxic than standard antisense oligonucleotides.
XX DAP or its analogues are more effective than other substitutes of
XX adenosine. The present sequence represents a sense oligonucleotide
XX used in the examples of the present invention.
XX
SQ Sequence 19 BP; 4 A; 10 C; 3 G; 2 T; 0 other;

QY 1 GGGTCTGCAGCGGATGCT 19
   |||||
Db 19 GGGTCTGCAGCGGATGCT 1

RESULT 4
ABX12700
ID ABX12700 standard; DNA; 19 BP.
XX
XX AC ABX12700;
XX
XX 10-MAY-2003 (first entry)
XX
DE Human IL-3/IL-5/GM-CSF receptor DNA, antisense oligonucleotide 107A.
XX
XX Human; inflammation; 2',6'-diaminopurine; DAP; antisense therapy;
XX DAP-modified oligonucleotide; pulmonary disease; respiratory disease;
XX neurological disease; cardiovascular disease; rheumatological disease;
XX digestive disease; cutaneous disease; ophthalmological disease;
XX urinary system disease; pathogen infection; genetic disease; cancer;
XX airway; nose; pulmonary fibrosis; adult respiratory distress syndrome;
XX cystic fibrosis; chronic obstructive lung disease; chronic bronchitis;
XX eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis;
XX hypereosinophilia; cardiac; ophthalmological; cytostatic;
XX antiasthmatic; antiallergic; antiinflammatory; immunosuppressive;
XX atopic disease; neoplastic cell proliferation; antisense; IL-3; IL-5;
XX interleukin-3 receptor; interleukin-5 receptor; GM-CSF; ss.
XX
XX Homo sapiens.
XX
OS
XX
```

```
PN WO2003004511-A2.
XX
XX 16-JAN-2003.
XX
XX 08-JUL-2002; 2002WO-CA01046.
XX
XX 06-JUL-2001; 2001US-303071P.
XX
XX (TOP1-) TOPIGEN PHARM INC.
XX
XX Renzi P, Allam M, Allakhverdi Z;
XX
XX WPI; 2003-247944/24.
XX
XX Increasing in vivo efficacy of a nucleic acid molecule that is
XX administered to a mammal for inhibiting inflammation in mammals,
XX involves incorporating into the nucleic acid molecule at least one
XX nucleotide substitute
XX
XX Examples; Page 18; 63pp; English.
XX
XX The present invention relates to a method for increasing the in vivo
XX efficacy of oligonucleotides and inhibiting inflammation. The
XX oligonucleotides comprise at least one nucleotide substitute of
XX 2',6'-diaminopurine (DAP) and/or its analogue. The DAP nucleotide
XX substitutions are useful for increasing in vivo efficacy of a nucleic
XX acid molecule that is administered to a mammal. The DAP-modified
XX oligonucleotides are useful in antisense therapy for treating and/or
XX preventing pulmonary/respiratory diseases, neurological diseases,
XX cardiovascular diseases, rheumatological diseases, digestive diseases,
XX cutaneous diseases, ophthalmological diseases, urinary system diseases,
XX pathogen infections, genetic diseases, general inflammation and
XX cancers. The respiratory system disease is a sickness associated with
XX an inflammation of the lungs, the airways and/or the nose. The
XX respiratory system disease is selected from pulmonary fibrosis, adult
XX respiratory distress syndrome, cystic fibrosis, chronic obstructive
XX lung disease, chronic bronchitis, eosinophilic bronchitis, asthma,
XX allergy, allergic rhinitis, sinusitis and hypereosinophilia. The
XX DAP-modified oligonucleotides are more stable in the body, more
XX effective, and less toxic than standard antisense oligonucleotides.
XX DAP or its analogues are more effective than other substitutes of
XX adenosine. The present sequence represents an antisense oligonucleotide
XX used in the examples of the present invention.
XX
SQ Sequence 19 BP; 2 A; 3 C; 10 G; 4 T; 0 other;

QY 1 GGGTCTGCAGCGGATGCT 19
   |||||
Db 1 GGGTCTGCAGCGGATGCT 19

RESULT 5
AAS70201/C
ID AAS70201 standard; cDNA; 619 BP.
XX
XX AC AAS70201;
XX
XX 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #6005.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
PD
```

XX 30-MAR-2001; 2001WO-US08631.
PF
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR P-PSDB; ABG06014.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 1, SEQ ID No 6005; 103pp; English.
PS
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 619 BP; 121 A; 203 C; 182 G; 113 T; 0 other;

Query Match 100.0%; Score 19; DB 23; Length 619;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
DB 336 GGGTCTGCAGCGGATGCT 318
|||||

RESULT 6
AAD51325/c
ID AAD51325 standard; cDNA; 3394 BP.
XX
AC AAD51325;
XX
DT 16-APR-2003 (first entry)
XX
DE Human receptor cDNA.
XX
KW Human; receptor; leukaemia; cancer; gene therapy; gene; ss.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT 5'UTR 1..188
FT CDS /*tag= a
FT 189..2273
FT /*tag= b
FT /product= "Human receptor"

FT 3'UTR 2274..3394
FT /*tag= c
XX
XX WO200292835-A2.
XX
XX 21-NOV-2002.
XX
XX 07-MAY-2002; 2002WO-US14274.
PF
XX 10-MAY-2001; 2001US-0851985.
PR
XX (PEKE) PE CORP NY.
PA
XX
PI Gong F, Yan C, Di Francesco V, Beasley EM;
XX
XX WPI; 2003-129304/12.
DR
DR P-PSDB; AAE33203.
XX
XX New human receptor proteins, useful for preparing a composition for
PT treating a disease or condition mediated by a human receptor protein
PT e.g., leukemia or cancer -
PT
XX
PS Claim 4; Fig 1A; 39pp; English.
PS
XX The invention relates to novel human receptor proteins and nucleic acid
CC molecules encoding such proteins. The invention is useful for preparing
CC a composition for treating a disease or condition mediated by a human
CC receptor protein e.g. leukemia or cancer. The invention is also useful
CC in gene therapy. The present sequence is human receptor cDNA.
XX
SQ Sequence 3394 BP; 713 A; 1011 C; 927 G; 743 T; 0 other;

Query Match 100.0%; Score 19; DB 25; Length 3394;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGCT 19
DB 285 GGGTCTGCAGCGGATGCT 267
|||||

RESULT 7
ABX63546/c
ID ABX63546 standard; cDNA; 3439 BP.
XX
AC ABX63546;
XX
DT 26-FEB-2003 (first entry)
XX
DE Human cDNA #546 differentially expressed in activated vascular tissue.
XX
XX Human; gene; ss; vascular tissue; cytosolic; atherosclerosis;
KW cardiac; hypotensive; antidiabetic; gynaecological; vasotropic;
KW cerebroprotective; gene therapy; vascular disease; cancer; coronary;
KW artery disease; hypertension; diabetes; pre-eclampsia; restenosis;
KW ischaemia-reperfusion injury; stroke;
XX
XX Homo sapiens.
OS
XX
XX US2002137081-A1.
PN
XX
XX 26-SEP-2002.
PD
XX
PF 08-JAN-2002; 2002US-0044090.
XX
PR 28-JUL-2000; 2000US-222469P.
PR 08-JAN-2001; 2001US-260483P.
XX
PA (BAND/) BANDMAN O.
XX
PI Bandman O;
XX
DR WPI; 2003-110597/10.

XX Combination for diagnosing, staging, treating, or monitoring the
PT progression of treatment of a vascular disease, e.g. atherosclerosis,
PT comprises several cDNAs that are differentially expressed in activated
PT vascular tissue -
XX
PS Claim 1; Page -, 18pp; English.
XX
CC This invention relates to a combination comprising several cDNAs that
CC are differentially expressed in activated vascular tissue. The invention
CC also discloses a high throughput method for detecting differentially
CC expressed cDNAs in a sample. The cDNAs of the invention may have
CC antiarteriosclerotic; cytoskeletal; cardiant; hypotensive; antidiabetic;
CC gynaecological; vasotropic and cerebroprotective activities and may be
CC used in gene therapy. The cDNAs of the invention may be used in a
CC high-throughput methods for detecting differential expression of one or
CC more cDNAs in a sample, or screening several molecules or compounds to
CC identify a molecule or compound that specifically binds a cDNA of the
CC invention. A protein encoded by the cDNA may be used to screen several
CC molecules or compounds to identify a ligand that specifically binds to
CC the protein, or to produce or purify an antibody to the protein that can
CC be used to detect a protein in a sample or purify a natural or
CC recombinant protein from a sample. The nucleotides may be useful for
CC diagnosing, staging, treating, or monitoring the progression of
CC treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary
CC artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-
CC reperfusion injury, restenosis, or stroke. The cDNAs can also be used
CC for large-scale genetic or gene expression analysis of several new
CC nucleic acid molecules. Antibodies to the proteins encoded by the
CC cDNAs are useful for diagnosing pre-pathologic disorders, and chronic
CC or acute diseases associated with abnormalities in the expression,
CC amount or distribution of the protein. The present sequence
CC represents a cDNA of the invention that is differentially expressed in
CC activated vascular tissue.
CC Note: The sequence data for this patent did not form part of the
CC specification, but was obtained in electronic format directly from USPTO
CC at <http://seqdata.uspto.gov/sequence.html?DocID=20020137081>.
XX
SQ Sequence 3439 BP; 675 A; 1122 C; 999 G; 643 T; 0 other;

Query Match 100.0%; Score 19; DB 25; Length 3439;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGGT 19
|||
Db 273 GGGTCTGCAGCGGATGGT 255

RESULT 8
AAQ21453/c
ID AAQ21453 standard; DNA; 3475 BP.
XX
AC AAQ21453;
XX
DT 17-MAY-1992 (first entry)
XX
DE Sequence encoding beta-chain of a human granulocyte-macrophage
DE colony stimulating factor (GM-CSF) receptor.
XX
XX Agonist; antagonist; myeloid leukaemia; therapy; screening;
KW diagnosis; granulocyte-macrophage colony stimulating factor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 201..2846
FT /*tag= a
XX
PN WO9201788-A.
XX
PD 06-FEB-1992.
XX

PF 16-JUL-1991; 91WO-US04846.
XX
PR 18-JUL-1990; 90US-0554745.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hayashida K, Kitamura T, Miyajima A;
XX
DR WPI; 1992-064947/08.
DR P-PSDB; AAR20982.
XX
XX Beta-chain of human granulocyte-macrophage CSF receptor - used
PT for screening agonists and antagonists of human GM-CSF, e.g. for
PT diagnosing myeloid leukaemia
XX
PS Claim 6; Page 13-14; 26pp; English.
XX
CC The nucleic acid encoding the human GM-CSF beta-chain is isolated
CC from a cDNA library prep'd. from poly(A)+ RNA from TF-1 cells. The
CC high affinity human GM-CSF receptor (Kd < 1 nM) can be used for
CC screening candidate GM-CSF agonists and antagonists e.g. for
CC treating myeloid leukaemias.
XX
SQ Sequence 3475 BP; 685 A; 1135 C; 1001 G; 654 T; 0 other;

Query Match 100.0%; Score 19; DB 13; Length 3475;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGGT 19
|||
Db 297 GGGTCTGCAGCGGATGGT 279

RESULT 9
AAD51326/c
ID AAD51326 standard; DNA; 21968 BP.
XX
AC AAD51326;
XX
DT 16-APR-2003 (first entry)
XX
DE Human receptor gene.
XX
KW Human; receptor; leukaemia; cancer; gene therapy; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace (183, T)
FT /*tag= a
FT /standard name= "Single nucleotide polymorphism"
FT replace (312, T)
FT /*tag= b
FT /standard name= "Single nucleotide polymorphism"
FT /*tag= c
FT /standard name= "Single nucleotide polymorphism"
FT replace (1449, A, G)
FT /*tag= d
FT /standard name= "Single nucleotide polymorphism"
FT replace (1453, A)
FT /*tag= e
FT /standard name= "Single nucleotide polymorphism"
FT 2176..19200
FT /*tag= f
FT /product= "Human receptor"
FT 2176..2251
FT /*tag= g
FT exon 2252..3211
FT /*tag= h
FT intron
FT variation replace (2441, C)
FT /*tag= i

FT		/standard name= "Single nucleotide polymorphism"
FT	variation	replace (2705, C)
FT		/ <tag= j<="" td=""></tag=>
FT		/standad name= "Single nucleotide polymorphism"
FT	variation	replace (2935, A)
FT		/ <tag= k<="" td=""></tag=>
FT		/standard name= "Single nucleotide polymorphism"
FT	variation	replace (3007, G)
FT		/ <tag= l<="" td=""></tag=>
FT		/standard name= "Single nucleotide polymorphism"
FT	exon	3212..3335
FT		/ <tag= m<="" td=""></tag=>
FT	intron	3336..5951
FT		/ <tag= n<="" td=""></tag=>
FT	variation	replace (5705, C)
FT		/ <tag= o<="" td=""></tag=>
FT		/standard name= "Single nucleotide polymorphism"
FT	variation	replace (5783, G)
FT		/ <tag= p<="" td=""></tag=>
FT		/standard name= "Single nucleotide polymorphism"
FT	exon	5952..6142
FT		/ <tag= q<="" td=""></tag=>
FT	intron	6143..9366
FT		/ <tag= r<="" td=""></tag=>
FT	variation	replace (6905, -)
FT		/ <tag= s<="" td=""></tag=>
FT		/standard name= "Single nucleotide polymorphism"
FT	variation	replace (7443, -)
FT		/ <tag= t<="" td=""></tag=>
FT		/standard name= "Single nucleotide polymorphism"
FT	variation	replace (7445, -)
FT		/ <tag= td="" u<=""></tag=>
FT		/standard name= "Single nucleotide polymorphism"
FT	variation	replace (7561, T)
FT		/ <tag= td="" v<=""></tag=>
FT		/standard name= "Single nucleotide polymorphism"
FT	variation	replace (7911, C)
FT		/ <tag= td="" w<=""></tag=>
FT		/standard_name= "Single nucleotide polymorphism"
FT	exon	9367..9524
FT		/ <tag= td="" x<=""></tag=>
FT	variation	replace (9427, -)
FT		/ <tag= td="" y<=""></tag=>
FT		/strand name= "Single nucleotide polymorphism"
FT	intron	9525..9603
FT		/ <tag= td="" z<=""></tag=>
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FT		/ <tag= aa<="" td=""></tag=>
FT		9773..10339
FT	intron	/ <tag= ab<="" td=""></tag=>
FT		10340..10475
FT	exon	/ <tag= ac<="" td=""></tag=>
FT		10476..10637
FT	intron	/ <tag= ad<="" td=""></tag=>
FT		10638..10795
FT	exon	/ <tag= ae<="" td=""></tag=>
FT		10796..12729
FT	intron	/ <tag= af<="" td=""></tag=>
FT		12730..12869
FT	exon	/ <tag= ag<="" td=""></tag=>
FT		12870..13796
FT	intron	/ <tag= ah<="" td=""></tag=>
FT	variation	replace (13599, T)
FT		/ <tag= ai<="" td=""></tag=>
FT		/standard name= "Single nucleotide polymorphism"
FT	exon	13797..13959
FT		/ <tag= aj<="" td=""></tag=>
FT	variation	replace (13922, C)
FT		/ <tag= ak<="" td=""></tag=>
FT		/standard name= "Single nucleotide polymorphism"
FT	intron	13960..15315
FT		/ <tag= al<="" td=""></tag=>
FT	variation	replace (14005, C)

FT	/tag= am
PT	/standard name= "Single nucleotide polymorphism"
FT	replace (I4702, C)
FT	/tag= an
FT	/standard name= "Single nucleotide polymorphism"
FT	replace (I5228, G)
PT	/tag= ao
PT	/standard name= "Single nucleotide polymorphism"
PT	15316..15406
PT	/tag= ap
PT	15407..15595
PT	/tag= aq
PT	15596..15653
PT	/tag= ar
PT	15654..16515
PT	/tag= as
PT	16516..16619
PT	/tag= at
PT	16620..17343
PT	/tag= au
PT	17344..17513
PT	/tag= av
PT	17514..18853
PT	/tag= aw
PT	18854..19200
PT	/tag= ax
PT	replace (I9251, C)
PT	/tag= ay
PT	/standard name= "Single nucleotide polymorphism"
PT	replace (I21335, C)
PT	/tag= az
PT	/standard name= "Single nucleotide polymorphism"
PT	replace (I21698, G)
PT	/tag= ba
PT	/standard_name= "Single nucleotide polymorphism"
PX	
PN	WO200292835-A2.
PX	
PD	21-NOV-2002.
PX	
PF	07-MAY-2002; 2002WO-US14274.
PX	
PR	10-MAY-2001; 2001US-0851985.
PX	
PA	(PEKE) PE CORP NY.
PX	
PI	Gong F, Yan C, Di Francesco V, Beasley EM;
PX	
DR	WPI; 2003-129304/12.
DR	P-PSTB; AAE33203.
PX	
PT	New human receptor proteins, useful for preparing a composition for
PT	treating a disease or condition mediated by a human receptor protein
PT	e.g., leukemia or cancer -
PX	
PS	Claim 4; Fig 3; 39pp; English.
PX	
CC	The invention relates to novel human receptor proteins and nucleic acid
CC	molecules encoding such proteins. The invention is useful for preparing
CC	a composition for treating a disease or condition mediated by a human
CC	receptor protein e.g. leukaemia or cancer. The invention is also useful
CC	in gene therapy. The present sequence is human receptor gene.
PX	
SQ	Sequence 21968 BP; 4659 A; 5655 C; 5769 G; 5017 T; 868 other;

Query Match	100.0%;	Score 19;	DB 25;	Length 21968;
Best Local Similarity	100.0%;	Pred. No. 15;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GGGTCTGCAGCGGATGT	19	
Db	3232	GGGTCTGCAGCGGATGT	3214	

RESULT 10
ABK83560/c
ID ABK83560 standard; cDNA, 86574 BP.
XX
AC ABK83560;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #131.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN WO200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30821.
XX
PR 03-OCT-2000; 2000US-237189P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
PS Claim 1; SEQ ID No 131; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a tissue having
CC or sterile inflammatory disease, by contacting a subject to a pathogen
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation (especially chronic) in a tissue, an allergic
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease, also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is

CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 86574 BP; 22071 A; 20398 C; 21552 G; 22553 T; 0 other;
SQ
Query Match 100.0%; Score 19; DB 24; Length 86574;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GGGTCGACGCGGATGCT 19
Db 74634 GGGTCGACGCGGATGCT 74616
GGGTCGACGCGGATGCT
RESULT 11
AAZ56194
ID AAZ56194 standard; DNA, 19 BP.
XX
AC AAZ56194;
XX
DT 28-MAR-2000 (first entry)
XX
DE Oligonucleotide 106 for IL-3/IL-5/GM-CSF receptor expression inhibition.
XX
KW Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
KW asthma; allergy; cancer; receptor expression inhibitor; cytokine;
KW inflammation; hypereosinophilia; eosinophil proliferation;
KW granulocyte macrophage colony stimulating factor; GM-CSF; ss.
XX
OS Homo sapiens.
XX
PN WO966037-A2.
XX
PD 23-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA00572.
XX
PR 17-JUN-1998; 98CA-2235420.
XX
PA (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
XX
PI Renzi P;
XX
DR WPI; 2000-097743/08.
XX
PT Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT macrophage colony stimulating factor receptors, used for treating or
PT preventing asthma, allergies, hypereosinophilia, inflammation or cancer
PT -
XX
PS Claim 5; Page 25; 72pp; English.
XX
CC This is an antisense oligonucleotide directed against the common beta
CC subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
CC receptor and the granulocyte macrophage colony stimulating factor
CC (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC involved in eosinophil proliferation and survival, they are increased in
CC asthma and atopic diseases, and are also involved in the indefinite
CC proliferation of certain neoplastic diseases. The invention relates to
CC antisense oligonucleotides directed against a nucleic acid sequence
CC encoding either a chemokine receptor (CCR3), a common subunit of
CC interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC oligonucleotides can be used in the treatment or prevention of asthma,
CC allergy, hypereosinophilia, general inflammation or cancer.
XX
SQ Sequence 19 BP; 2 A; 3 C; 9 G; 5 T; 0 other;

Query Match 94.7%; Score 18; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGCTGCAGCGGATGCT 19
DB 1 GGCTGCAGCGGATGCT 18

RESULT 12
AAZ56195
ID AAZ56195 standard; DNA; 19 BP.

AAZ56195;

28-MAR-2000 (first entry)

Oligonucleotide 108 for IL-3/IL-5/GM-CSF receptor expression inhibition.

Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
asthma; allergy; cancer; receptor expression inhibitor; cytokine;
inflammation; hypereosinophilia; eosinophil proliferation;
granulocyte macrophage colony stimulating factor; GM-CSF; ss.

Homo sapiens.

WO9966037-A2.

23-DEC-1999.

17-JUN-1999; 99WO-CA00572.

17-JUN-1998; 98CA-2235420.

(REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.

Renzi P;

WPI; 2000-097743/08.

Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
macrophage colony stimulating factor receptors, used for treating or
preventing asthma, allergies, hypereosinophilia, inflammation or cancer

Claim 5; Page 25; 72pp; English.

This is an antisense oligonucleotide directed against the common beta
subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
receptor and the granulocyte macrophage colony stimulating factor
(GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
involved in eosinophil proliferation and survival, they are increased in
asthma and atopic diseases, and are also involved in the indefinite
proliferation of certain neoplastic diseases. The invention relates to
antisense oligonucleotides directed against a nucleic acid sequence
encoding either a chemokine receptor (CCR3), a common subunit of
interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
oligonucleotides can be used in the treatment or prevention of asthma,
allergy, hypereosinophilia, general inflammation or cancer.

Sequence 19 BP; 3 A; 3 C; 10 G; 3 T; 0 other;

Query Match 94.7%; Score 18; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGCTCTGCAGCGGATGG 18
DB 2 GGCTCTGCAGCGGATGG 19

RESULT 13
ABX12689
ID ABX12689 standard; DNA; 19 BP.

ABX12689;

10-MAY-2003 (first entry)

Human IL-3/IL-5/GM-CSF receptor DNA, antisense oligonucleotide #2.

Human; inflammation; 2',6'-diaminopurine; DAP; antisense therapy;
DAP-modified oligonucleotide; pulmonary disease; respiratory disease;
neurological disease; cardiovascular disease; rheumatological disease;
digestive disease; cutaneous disease; ophthalmological disease;
urinary system disease; pathogen infection; genetic disease; cancer;
airway; nose; pulmonary fibrosis; adult respiratory distress syndrome;
cystic fibrosis; chronic obstructive lung disease; chronic bronchitis;
eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis;
hypereosinophilia; cardiac; ophthalmological; cytostatic;
antiasthmatic; antiallergic; antiinflammatory; immunosuppressive;
atopic disease; neoplastic cell proliferation; antisense; IL-3; IL-5;
interleukin-3 receptor; interleukin-5 receptor; GM-CSF; ss.

Homo sapiens.

WO2003004511-A2.

16-JAN-2003.

08-JUL-2002; 2002WO-CA01046.

06-JUL-2001; 2001US-303071P.

(TOPI-) TOPIGEN PHARM INC.

Renzi P, Allam M, Allakherdi Z;

WPI; 2003-247944/24.

Increasing in vivo efficacy of a nucleic acid molecule that is
administered to a mammal for inhibiting inflammation in mammals,
involves incorporating into the nucleic acid molecule at least one
nucleotide substitute

Claim 28; Page 11; 63pp; English.

The present invention relates to a method for increasing the in vivo
efficacy of oligonucleotides and inhibiting inflammation. The
oligonucleotides comprise at least one nucleotide substitute of
2',6'-diaminopurine (DAP) and/or its analogue. The DAP nucleotide
substitutions are useful for increasing in vivo efficacy of a nucleic
acid molecule that is administered to a mammal. The DAP-modified
oligonucleotides are useful in antisense therapy for treating and/or
preventing pulmonary/respiratory diseases, neurological diseases,
cardiovascular diseases, ophthalmological diseases, digestive diseases,
cutaneous diseases, genetic diseases, general inflammation and
cancers. The respiratory system disease is a sickness associated with
an inflammation of the lungs, the airways and/or the nose. The
respiratory system disease is selected from pulmonary fibrosis, adult
respiratory distress syndrome, cystic fibrosis, chronic obstructive
lung disease, chronic bronchitis, eosinophilic bronchitis, asthma,
allergy, allergic rhinitis, sinusitis and hypereosinophilia. The
DAP-modified oligonucleotides are more stable in the body, more
effective, and less toxic than standard antisense oligonucleotides.
DAP or its analogues are more effective than other substitutes of
adenosine. ABX12681-ABX12698 represent antisense oligonucleotides
for treating or preventing atopic diseases and neoplastic cell
proliferation.

Sequence 19 BP; 2 A; 3 C; 9 G; 5 T; 0 other;

Query Match 94.7%; Score 18; DB 25; Length 19;

Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GGCTGCAGCGGATGT 19
|||
Db 1 GGCTGCAGCGGATGT 18

RESULT 14
ABX12690
ID ABX12690 standard; DNA; 19 BP.

XX AC ABX12690;

DT 10-MAY-2003 (first entry)

DE Human IL-3/IL-5/GM-CSF receptor DNA, antisense oligonucleotide #3.

XX Human; inflammation; 2'6'-diaminopurine; DAP; antisense therapy;
KW DAP-modified oligonucleotide; pulmonary disease; respiratory disease;
KW neurological disease; cardiovascular disease; rheumatological disease;
KW digestive disease; cutaneous disease; ophthalmological disease;
KW urinary system disease; pathogen infection; genetic disease; cancer;
KW airway; nose; pulmonary fibrosis; adult respiratory distress syndrome;
KW cystic fibrosis; chronic obstructive lung disease; chronic bronchitis;
KW eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis;
KW hyper eosinophilia; cardiant; ophthalmological; cytostatic;
KW antiasthmatic; anti allergic; anti inflammatory; immunosuppressive;
KW atopic disease; neoplastic cell proliferation; antisense; IL-3; IL-5;
KW interleukin-3 receptor; interleukin-5 receptor; GM-CSF; ss.

XX OS Homo sapiens.

XX PN WO2003004511-A2.

XX PD 16-JAN-2003.

XX PF 08-JUL-2002; 2002WO-CA01046.

XX PR 06-JUL-2001; 2001US-303071P.

XX PA (TOPI-) TOPIGEN PHARM INC.

XX PI Renzi P, Allam M, Allakhverdi Z;

XX DR WPI; 2003-247944/24.

XX PT Increasing in vivo efficacy of a nucleic acid molecule that is
PT administered to a mammal for inhibiting inflammation in mammals,
PT involves incorporating into the nucleic acid molecule at least one
PT nucleotide substitute -

XX PS Claim 28; Page 11; 63pp; English.

XX The present invention relates to a method for increasing the in vivo
CC efficacy of oligonucleotides and inhibiting inflammation. The
CC oligonucleotides comprise at least one nucleotide substitute of
CC 2'6'-diaminopurine (DAP) and/or its analogue. The DAP nucleotide
CC substitutions are useful for increasing in vivo efficacy of a nucleic
CC acid molecule that is administered to a mammal. The DAP-modified
CC oligonucleotides are useful in antisense therapy for treating and/or
CC preventing pulmonary/respiratory diseases, neurological diseases,
CC cardiovascular diseases, rheumatological diseases, digestive diseases,
CC cutaneous diseases, ophthalmological diseases, urinary system diseases,
CC pathogen infections, genetic diseases, general inflammation and
CC cancers. The respiratory system disease is a sickness associated with
CC an inflammation of the lungs, the airways and/or the nose. The
CC respiratory system disease is selected from pulmonary fibrosis, adult
CC respiratory distress syndrome, cystic fibrosis, chronic obstructive
CC lung disease, chronic bronchitis, eosinophilic bronchitis, asthma,
CC allergy, allergic rhinitis, sinusitis and hyper eosinophilia. The
CC DAP-modified oligonucleotides are more stable in the body, more
CC effective, and less toxic than standard antisense oligonucleotides.

CC DAP or its analogues are more effective than other substitutes of
CC adenosine. ABX12681-ABX12698 represent antisense oligonucleotides
CC for treating or preventing atopic diseases and neoplastic cell
CC proliferation.

XX SQ Sequence 19 BP; 3 A; 3 C; 10 G; 3 T; 0 other;

Query Match 94.7%; Score 18; DB 25; Length 19;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGCTGCAGCGGATCG 18
|||
Db 2 GGCTGCAGCGGATCG 19

RESULT 15
AAZ56199
ID AAZ56199 standard; DNA; 19 BP.

XX AC AAZ56199;

DT 28-MAR-2000 (first entry)

DE Oligonucleotide 105 for IL-3/IL-5/GM-CSF receptor expression inhibition.

XX Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
KW asthma; allergy; cancer; receptor expression inhibitor; cytokine;
KW inflammation; hyper eosinophilia; eosinophil proliferation;
KW granulocyte macrophage colony stimulating factor; GM-CSF; ss.

XX OS Homo sapiens.

XX PN WO9966037-A2.

XX PD 23-DEC-1999.

XX PF 17-JUN-1999; 99WO-CA00572.

XX PR 17-JUN-1998; 98CA-2235420.

XX PA (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.

XX PI Renzi P;

XX DR WPI; 2000-097743/08.

XX PT Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT macrophage colony stimulating factor receptors, used for treating or
PT preventing asthma, allergies, hyper eosinophilia, inflammation or cancer

XX PS Claim 5; Page 25; 72pp; English.

XX This is an antisense oligonucleotide directed against the common beta
CC subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
CC receptor and the granulocyte macrophage colony stimulating factor
CC (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC involved in eosinophil proliferation and survival, they are increased in
CC asthma and atopic diseases, and are also involved in the indefinite
CC proliferation of certain neoplastic diseases. The invention relates to
CC antisense oligonucleotides directed against a nucleic acid sequence
CC encoding either a chemokine receptor (CCR3), a common subunit of
CC interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC oligonucleotides can be used in the treatment or prevention of asthma,
CC allergy, hyper eosinophilia, general inflammation or cancer.

XX SQ Sequence 19 BP; 2 A; 3 C; 8 G; 6 T; 0 other;

Query Match 89.5%; Score 17; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;

```
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GTCTGCAGCGGATGGT 19
   |||||
   1 GTCTGCAGCGGATGGT 17
DB

RESULT 16
ABX12694
ID ABX12694 standard; DNA, 19 BP.
XX
AC ABX12694;
XX
DT 10-MAY-2003 (first entry)
XX
DE Human IL-3/IL-5/GM-CSF receptor DNA, antisense oligonucleotide #7.
XX
KW Human; inflammation; 2'6'-diaminopurine; DAP; antisense therapy;
KW DAP-modified oligonucleotide; pulmonary disease; respiratory disease;
KW neurological disease; cardiovascular disease; rheumatological disease;
KW digestive disease; cutaneous disease; ophthalmological disease;
KW urinary system disease; pathogen infection; genetic disease; cancer;
KW airway; nose; pulmonary fibrosis; adult respiratory distress syndrome;
KW cystic fibrosis; chronic obstructive lung disease; chronic bronchitis;
KW eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis;
KW hyper eosinophilia; cardiant; ophthalmological; cytostatic;
KW antiasthmatic; antiallergic; antiinflammatory; immunosuppressive;
KW atopic disease; neoplastic cell proliferation; antisense; IL-3; IL-5;
KW interleukin-3 receptor; interleukin-5 receptor; GM-CSF; ss.
XX
OS Homo sapiens.
XX
PN WO2003004511-A2.
XX
PD 16-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-CA01046.
XX
PR 06-JUL-2001; 2001US-303071P.
XX
PA (TOPI-) TOPIGEN PHARM INC.
XX
PI Renzi P, Allam M, Allakhverdi Z;
XX
DR WPI; 2003-247944/24.
XX
PT Increasing in vivo efficacy of a nucleic acid molecule that is
PT administered to a mammal for inhibiting inflammation in mammals,
PT involves incorporating into the nucleic acid molecule at least one
PT nucleotide substitute -
XX
PS Claim 28; Page 11; 63pp; English.
XX
CC The present invention relates to a method for increasing the in vivo
CC efficacy of oligonucleotides and inhibiting inflammation. The
CC oligonucleotides comprise at least one nucleotide substitute of
CC 2'6'-diaminopurine (DAP) and/or its analogue. The DAP nucleotide
CC substitutions are useful for increasing in vivo efficacy of a nucleic
CC acid molecule that is administered to a mammal. The DAP-modified
CC oligonucleotides are useful in antisense therapy for treating and/or
CC preventing pulmonary/respiratory diseases, neurological diseases,
CC cardiovascular diseases, rheumatological diseases, digestive diseases,
CC cutaneous diseases, ophthalmological diseases, urinary system diseases,
CC pathogen infections, genetic diseases, general inflammation and
CC cancers. The respiratory system disease is a sickness associated with
CC an inflammation of the lungs, the airways and/or the nose. The
CC respiratory system disease is selected from pulmonary fibrosis, adult
CC respiratory distress syndrome, cystic fibrosis, chronic obstructive
CC lung disease, chronic bronchitis, eosinophilic bronchitis, asthma,
CC allergy, allergic rhinitis, sinusitis and hyper eosinophilia. The
CC DAP-modified oligonucleotides are more stable in the body, more
CC effective, and less toxic than standard antisense oligonucleotides.
CC DAP or its analogues are more effective than other substitutes of
```

```
CC adenosine. ABX12681-ABX12698 represent antisense oligonucleotides
CC for treating or preventing atopic diseases and neoplastic cell
CC proliferation.
XX
SQ Sequence 19 BP; 2 A, 3 C, 8 G, 6 T, 0 other;
QY 3 GTCTGCAGCGGATGGT 19
   |||||
   1 GTCTGCAGCGGATGGT 17
DB

Query Match      89.5%; Score 17; DB 25; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GTCTGCAGCGGATGGT 19
   |||||
   1 GTCTGCAGCGGATGGT 17
DB

RESULT 17
ABX12701
ID ABX12701 standard; DNA, 19 BP.
XX
AC ABX12701;
XX
DT 10-MAY-2003 (first entry)
XX
DE Human IL-3/IL-5/GM-CSF receptor DNA, antisense oligonucleotide 107A-DAP.
XX
KW Human; inflammation; 2'6'-diaminopurine; DAP; antisense therapy;
KW DAP-modified oligonucleotide; pulmonary disease; respiratory disease;
KW neurological disease; cardiovascular disease; rheumatological disease;
KW digestive disease; cutaneous disease; ophthalmological disease;
KW urinary system disease; pathogen infection; genetic disease; cancer;
KW airway; nose; pulmonary fibrosis; adult respiratory distress syndrome;
KW cystic fibrosis; chronic obstructive lung disease; chronic bronchitis;
KW eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis;
KW hyper eosinophilia; cardiant; ophthalmological; cytostatic;
KW antiasthmatic; antiallergic; antiinflammatory; immunosuppressive;
KW atopic disease; neoplastic cell proliferation; antisense; IL-3; IL-5;
KW interleukin-3 receptor; interleukin-5 receptor; GM-CSF; ss.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 9 /*tag= a
FT /*mod_base= OTHER
FT /note= "OTHER= DAP"
FT modified_base 15 /*tag= b
FT /*mod_base= OTHER
FT /note= "OTHER= DAP"
XX
PN WO2003004511-A2.
XX
PD 16-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-CA01046.
XX
PR 06-JUL-2001; 2001US-303071P.
XX
PA (TOPI-) TOPIGEN PHARM INC.
XX
PI Renzi P, Allam M, Allakhverdi Z;
XX
DR WPI; 2003-247944/24.
XX
PT Increasing in vivo efficacy of a nucleic acid molecule that is
PT administered to a mammal for inhibiting inflammation in mammals,
PT involves incorporating into the nucleic acid molecule at least one
PT nucleotide substitute -
XX
PS Examples; Page 18; 63pp; English.
XX
CC The present invention relates to a method for increasing the in vivo
```


CC efficacy of oligonucleotides and inhibiting inflammation. The
CC oligonucleotides comprise at least one nucleotide substitute of
CC 2',6'-diaminopurine (DAP) and/or its analogue. The DAP nucleotide
CC substitutions are useful for increasing *in vivo* efficacy of a nucleic
CC acid molecule that is administered to a mammal. The DAP-modified
CC oligonucleotides are useful in antisense therapy for treating and/or
CC preventing pulmonary/respiratory diseases, neurological diseases,
CC cardiovascular diseases, rheumatological diseases, digestive diseases,
CC cutaneous diseases, ophthalmological diseases, urinary system diseases,
CC pathogen infections, genetic diseases, general inflammation and
CC cancers. The respiratory system disease is a sickness associated with
CC an inflammation of the lungs, the airways and/or the nose. The
CC respiratory system disease is selected from pulmonary fibrosis, adult
CC respiratory distress syndrome, cystic fibrosis, chronic obstructive
CC lung disease, chronic bronchitis, eosinophilic bronchitis, asthma,
CC allergy, allergic rhinitis, sinusitis and hyper eosinophilia. The
CC DAP-modified oligonucleotides are more stable in the body, more
CC effective, and less toxic than standard antisense oligonucleotides.
CC DAP or its analogues are more effective than other substitutes of
CC adenosine. The present sequence represents an antisense oligonucleotide
CC used in the examples of the present invention.

SQ Sequence 19 BP; 0 A; 3 C; 10 G; 4 T; 2 other;

Query Match	89.5%	Score 17;	DB 25;	Length 19;
Best Local Similarity	89.5%	Pred. No. 91;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

QY 1 GGGTCTGCAGCGGATGCT 19
|||
Db 1 GGGTCTGCNCGCGGNTGCT 19

RESULT 18

ABX12702
ID ABX12702 standard; DNA; 19 BP.

AC ABX12702;

DT 10-MAY-2003 (first entry)

Human IL-3/IL-5/GM-CSF receptor DNA, antisense oligonucleotide 107A-I.

Human, inflammation; 2',6'-diaminopurine, DAP, antisense therapy; DAP-modified oligonucleotide; pulmonary disease; respiratory disease; neurological disease; cardiovascular disease; rheumatological disease; digestive disease; cutaneous disease; ophthalmological disease; urinary system disease; pathogen infection; genetic disease; cancer; airway; nose; pulmonary fibrosis; adult respiratory distress syndrome; cystic fibrosis; chronic obstructive lung disease; chronic bronchitis; eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis; hyper eosinophilia; cardiast; ophthalmological; cytostatic; antiaesthetic; antiallergic; antiinflammatory; immunosuppressive; atopic disease; neoplastic cell proliferation; antitense, IL-3; IL-5; interleukin-3 receptor; interleukin-5 receptor; GM-CSF, ss.

OS Homo sapiens.
OS Synthetic.

FT	Key	Location/Qualifiers
FT	modified_base	9
FT		/*tag= a
FT	modified_base	15
FT	modified_base	/*tag= b
FT		/mod_base= i
FT		

PN WO2003004511-A2.

PD 16-JAN-2003

PF 08-JUL-2002; 2002WO-CA01046.

PR 06-JUL-2001; 2001US-303071P.

PA (TOPI-) TOPIGEN PHARM INC.

PI Renzi P, Allam M, Allakhverdi Z;

DR WPI; 2003-247944/24.

PT Increasing in vivo efficacy of a nucleic acid molecule that is
PT administered to a mammal for inhibiting inflammation in mammals,
PT involves incorporating into the nucleic acid molecule at least one
PT nucleotide substitute -

PS Examples; Page 18; 63pp; English..

The present invention relates to a method for increasing the in vivo efficacy of oligonucleotides and inhibiting inflammation. The oligonucleotides comprise at least one nucleotide substitute of 2',6'-diaminopurine (DAP) and/or its analogue. The DAP nucleotide substitutions are useful for increasing in vivo efficacy of a nucleic acid molecule that is administered to a mammal. The DAP-modified oligonucleotides are useful in antisense therapy for treating and/or preventing pulmonary/respiratory diseases, neurological diseases, cardiovascular diseases, rheumatological diseases, digestive diseases, cutaneous diseases, ophthalmological diseases, urinary system diseases, pathogen infections, genetic diseases, general inflammation and cancers. The respiratory system disease is a sickness associated with an inflammation of the lungs, the airways and/or the nose. The respiratory system disease is selected from pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis, chronic obstructive lung disease, chronic bronchitis, eosinophilic bronchitis, asthma, allergy, allergic rhinitis, sinusitis and hyperesinophilia. The DAP-modified oligonucleotides are more stable in the body, more effective, and less toxic than standard antisense oligonucleotides. DAP or its analogues are more effective than other substitutes of adenosine. The present sequence represents an antisense oligonucleotide used in the examples of the present invention.

Sequence 19 BP; 0 A; 3 C; 10 G; 4 T; 2 other;

Query Match	89.5%	Score 17;	DB 25;	Length 19;
Best Local Similarity	89.5%;	Pred. No. 91;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1 GGGTCTGCAGCGGATGCT 19
Db	1 GGCTCTGCNCGCGGNTGCT 19

RESULT 19
AAK63218/c

AC AAK63218;

DT	06-NOV-2001	(first entry)
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DE	Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:8278.
724	

Human; immune; haematopoietic; immune/haematopoietic antigen; cancer, cytostatic; gene therapy; vaccine; metastasis; ss.

05 Homo sapiens.

PN WO200157182-A2.

PD 09-AUG-2001

17-JAN-2001; 2001WO-US01354.

31-JAN-2000; 2000US-0179065.

PR 24-FEB-2000; 2000US-0184664.

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PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
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PR 14-AUG-2000; 2000US-0225758.
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PR 01-SEP-2000; 2000US-0229344.
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PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
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PR 29-SEP-2000; 2000US-0236327.
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PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.

PR 02-OCT-2000; 2000US-0237039.

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PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241826.
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PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
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PR 17-NOV-2000; 2000US-0249213.
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PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
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PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
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PR 05-DEC-2000; 2000US-0256719.
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PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX
XX DR MPI; 2001-483426/52.
XX DR P-PSDB; AAM90437.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Claim 1; SEQ ID NO 8278; 3071pp + Sequence Listing; English.
```

XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 256 BP; 67 A; 71 C; 71 G; 46 T; 1 other;
Query Match 86.3%; Score 16.4; DB 22; Length 256;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 GGGTCGACGGGATGCG 18
|||
Db 207 GGGTCGACGACGATGCG 190
RESULT 20
AAAF1002
ID AAF71002 standard; DNA; 436 BP.
XX
AC AAF71002;
XX
DT 30-APR-2001 (first entry)
XX
DE C. glutamicum SRT protein nucleotide sequence SEQ ID NO:37.
XX
KW Corynebacterium glutamicum; stress; resistance; tolerance; SRT;
KW fine chemical production; organic acid; proteinogenic amino acid;
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
KW evolutionary study; environmental hazard; fermentation; ds.
XX
OS Corynebacterium glutamicum.
XX
PN WO200100804-A2.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-IB00922.
XX
PR 25-JUN-1999; 99US-0141031.
PR 01-JUL-1999; 99DE-1030429.
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PR 08-JUL-1999; 99DE-1031413.
PR 08-JUL-1999; 99DE-1031457.
PR 08-JUL-1999; 99DE-1031541.
PR 09-JUL-1999; 99DE-1032209.
PR 09-JUL-1999; 99DE-1032230.
PR 14-JUL-1999; 99DE-1032914.
PR 27-AUG-1999; 99DE-1040764.
PR 27-AUG-1999; 99US-0151214.
PR 31-AUG-1999; 99DE-1041382.
XX
PA (BADI) BASF AG.
XX
PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Habernauer G, Lee H;
PI Kim H;
XX

DR WPI; 2001-061972/07.
DR P-PSDB; AAB78889.
XX
PT New isolated Corynebacterium glutamicum nucleic acid encoding a stress,
PT tolerance or resistance protein, for production or modulation of
PT production of fine chemicals, such as, e.g. amino acids, lipids,
PT carbohydrates, or enzymes -
XX
PS Claim 3; Page 172; 526pp; English.
XX
CC AAF70984 to AAF71133 encode the Corynebacterium glutamicum stress,
CC resistance, and tolerance (SRT) proteins given in AAB78871 to AAB79020.
CC The C. glutamicum SRT genes (I) can be used in vectors (II) for
CC expression in host cells and production of fine chemicals, such as, an
CC organic acid, a proteinogenic or nonproteinogenic amino acid (preferred),
CC a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a
CC saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic
CC compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine
CC chemical production can be modulated. The presence of (I) or the SRT
CC proteins (III) encoded by them are used for diagnosing the presence
CC or activity of Corynebacterium diphtheriae. (I), (II), (III) and host
CC cells containing them can be used to map the genomes of organisms related
CC to C. glutamicum, to identify and localise C. glutamicum sequences of
CC interest, in evolutionary studies, in determination of SRT protein
CC regions required for function, in modulating the SRT protein activity,
CC and in modulating the activity of an SRT pathway. (II) are used to permit
CC C. glutamicum to survive in an environment that is normally
CC environmentally or chemically hazardous to it. (I) and protein molecules
CC encoded by it increase the survival of C. glutamicum to chemical and
CC environmental hazards and provide a means for continued growth and
CC multiplication in large scale fermentative growth conditions. By
CC increasing the growth rate or maintaining a normal growth rate in poor or
CC toxic conditions, the yield, production and/or efficiency or production
CC of fine chemicals from a culture may be increased.
XX
SQ Sequence 436 BP; 81 A; 102 C; 138 G; 115 T; 0 other;
Query Match 86.3%; Score 16.4; DB 22; Length 436;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2 GGTCTGACGGGATGCT 19
|||
Db 401 GGTCTGACGGGAGCT 418
RESULT 21
AAK84431/c
ID AAK84431 standard; DNA; 535 BP.
XX
AC AAK84431;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39243.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosolic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
XX

PR 18-APR-2000; 2000US-0198123.
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PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
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PR 08-SEP-2000; 2000US-0232081.
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PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
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PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
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PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM,
PI
XX
XX WPI; 2001-483426/52.
DR
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
PT
XX
XX
PS Disclosure; SEQ ID NO 39243; 3071bp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosstatic
CC activity, and can be used in gene therapy and vaccine production. (I)

CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM62169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 535 BP; 148 A; 159 C; 143 G; 85 T; 0 other;

Query Match 86.3%; Score 16.4; DB 22; Length 535;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGG 18
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Db 206 GGGTCTGCAGCAGATGG 189

RESULT 22
AAK84430/c
ID AAK84430 standard; DNA; 536 BP.
XX
AC AAK84430;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39242.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
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PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
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PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 14-AUG-2000; 2000US-0225757.
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PR 23-AUG-2000; 2000US-0227009.
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PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
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PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
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PR 26-SEP-2000; 2000US-0235484.
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PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
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PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
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PR 02-OCT-2000; 2000US-0237040.
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PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.

PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 39242; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins, and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 536 BP; 146 A; 161 C; 143 G; 86 T; 0 other;

Query Match 86.3%; Score 16.4; DB 22; Length 536;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGTCTGCAGCGGATGG 18
DB 206 GGGTCTGCAGCGGATGG 189
RESULT 23
AAS67706
ID AAS67706 standard; cDNA; 825 BP.
XX
AC AAS67706;
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #3510.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG03519.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX
PS Claim 1; SEQ ID NO 3510; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 825 BP; 156 A; 278 C; 267 G; 124 T; 0 other;

Query Match 86.3%; Score 16.4; DB 23; Length 825;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGTCTGCAGCGGATGGT 19

Db 665 GGCTGCGACGGGACGGT 682

RESULT 24

AA583466

ID AA583466 standard; cDNA; 825 BP.

AC AA583466;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #19270.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR P-PSDB; AAB19279.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 1; SEQ ID No 19270; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AA584197-AA594564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 825 BP; 157 A; 285 C; 258 G; 125 T; 0 other;

SO Query Match 86.3%; Score 16.4; DB 23; Length 825;

Best Local Similarity 94.4%; Pred. No. 2.2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGCTGCGACGGGATGTT 19

Db 668 GGCTGCGACGGGACGGT 685

RESULT 25

AA72267/C

ID AA72267 standard; cDNA; 1095 BP.

AC AA72267;

DT 06-DEC-2000 (first entry)

DE Drosophila odorant receptor DORLU 1.1 cDNA.

KW Odorant receptor; Drosophila; olfactory receptor;

KW G protein-coupled receptor; GPCR superfamily; transgenic insect;

KW insect behaviour modification; pest control; pollinator attraction;

KW biosensor; odour detection; odour identification; apiculture; ss.

OS Drosophila melanogaster.

PN WO200043410-A2.

PD 27-JUL-2000.

PF 25-JAN-2000; 2000WO-US01823.

PR 25-JAN-1999; 99US-0117132.

PA (UYVA) UNIV YALE.

PI Carlson JR, Klm J, Clyne PJ, Warr CG;

DR WPI; 2000-543246/49.

DR P-PSDB; AAB20932.

PT New nucleic acid encoding a Drosophila olfactory receptor, useful for
PT identifying modulating agents -

PS Claim 3; Page 214-216; 303pp; English.

XX Sequences AA72236-A72284 represent cDNAs encoding Drosophila
CC melanogaster odorant receptors (AAB20901-B20949). These proteins function
CC as olfactory receptors, and are thought to be members of the G
CC protein-coupled receptor (GPCR) superfamily, which is characterised by
CC the presence of 7 transmembrane helices. Nucleic acids encoding the
CC Drosophila odorant receptors may be used to generate expression
CC constructs, host cells containing such constructs, and transgenic
CC insects. Cells which express the odorant receptor genes may be used in
CC methods to identify agents which modulate expression of these genes, and
CC in methods to identify receptor binding partners. The Drosophila odorant
CC receptor nucleic acids may also be used to identify corresponding genes
CC in other insects, such as those which damage crops or transmit disease.
CC The odorant receptor proteins may be used to identify agents which
CC modulate their activity, to identify binding partners, as antigens to
CC raise antibodies, and in methods to modify insect behaviour. The proteins
CC may be also be used in methods of behaviour modification. Such methods
CC such as pheromones. Modification of insect behaviour has a wide range of
CC applications, such as in pest control (e.g., by disrupting the feeding
CC or mating behaviours of pest species), or for enhancing plant
CC pollination (by attracting pollinator species). Odorant receptor proteins
CC and/or nucleotides may also be used to identify appetite suppressants, to
CC trap odours of a specific type, as biosensors for the detection of
CC explosives, drugs, perfumes or pollutants, and in apiculture to modify
CC the behaviour of bees, for example, to increase the production of royal
CC jelly.

XX Sequence 1095 BP; 210 A; 336 C; 273 G; 276 T; 0 other;

SO Query Match 86.3%; Score 16.4; DB 21; Length 1095;

Best Local Similarity 94.4%; Pred. No. 2.2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGCTGCGACGGGATGTT 19

PR 12-JAN-2001; 2001NO-0000235.
PR 12-JAN-2001; 2001NO-0000239.
XX
PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.
PA (TIGR-) TIGR.
XX
PI Birkeland NK, Eidhammer I, Jonassen I, Jensen HB, Lien T,
PI Lillehaug JR, Lossius I, Eisen JA, Fraser CM, Durkin AS,
PI Salzberg SL;
XX
DR WPI; 2002-557818/59.
XX
PT Novel DNA array useful for determining differential expression of
PT Methylococcus capsulatus genes, comprises polynucleotides or
PT oligonucleotides representative for a selective number of Methylococcus
PT capsulatus genes -
XX
PS Claim 19; Page 71-72; 678bp; English.
XX
CC The invention relates to a novel DNA array giving a representation of a
CC number of Methylococcus capsulatus genes. The method of the invention is
CC useful for determination of the differential expression of the genes of
CC M. capsulatus, and for studying gene expression on a genomic scale and in
CC gene expression assays of M. capsulatus genes. The sequences shown in
CC ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
CC invention.
XX
SQ Sequence 1320 BP; 276 A; 409 C; 399 G; 236 T; 0 other;
XX
Query Match 86.3%; Score 16.4; DB 24; Length 1320;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GGCTGCACGGGATGCT 19
|||
Db 876 GGCTGCACGGGATGCT 859
|||
RESULT 29.
ABQ90381
ID ABQ90381 standard; DNA; 1443 BP.
XX
AC ABQ90381;
XX
DT 01-OCT-2002 (first entry)
XX
DE M. capsulatus gene #366 for DNA array.
XX
KW Micro array; gene; ds; differential expression; gene expression.
XX
OS Methylococcus capsulatus.
XX
PN WO200255655-A2.
XX
PD 18-JUL-2002.
XX
PE 14-JAN-2002; 2002WO-NO00019.
XX
PR 12-JAN-2001; 2001NO-0000235.
PR 12-JAN-2001; 2001NO-0000239.
XX
PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.
PA (TIGR-) TIGR.
XX
PI Birkeland NK, Eidhammer I, Jonassen I, Jensen HB, Lien T,
PI Lillehaug JR, Lossius I, Eisen JA, Fraser CM, Durkin AS,
PI Salzberg SL;
XX
DR WPI; 2002-557818/59.
XX
PT Novel DNA array useful for determining differential expression of
PT Methylococcus capsulatus genes, comprises polynucleotides or
PT oligonucleotides representative for a selective number of Methylococcus

PT capsulatus genes -
XX
PS Claim 19; Page 224-225; 678bp; English.
XX
CC The invention relates to a novel DNA array giving a representation of a
CC number of Methylococcus capsulatus genes. The method of the invention is
CC useful for determination of the differential expression of the genes of
CC M. capsulatus, and for studying gene expression on a genomic scale and in
CC gene expression assays of M. capsulatus genes. The sequences shown in
CC ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
CC invention.
XX
SQ Sequence 1443 BP; 259 A; 439 C; 447 G; 298 T; 0 other;
XX
Query Match 86.3%; Score 16.4; DB 24; Length 1443;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GGCTGCACGGGATGCT 19
|||
Db 496 GGCTGCACGGGATGCT 513
|||
RESULT 30
AAC79967/C
ID AAC79967 standard; cDNA; 1537 BP.
XX
AC AAC79967;
XX
DT 12-FEB-2001 (first entry)
XX
DE Human secreted protein encoding cDNA for gene 20.
XX
KW Secreted protein; human; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW nootropic; neuroprotective; antibacterial; virucide; fungicide;
KW ophthalmological; vulnerary; gene therapy; treatment; autoimmune disease;
KW hyperproliferative disorder; cardiovascular disorder; ocular disorder;
KW cerebrovascular disorder; nervous system disorder; infection; skin aging;
KW wound healing; epithelial cell proliferation; transplantation; ss.
XX
OS Homo sapiens.
XX
PN WO200058357-A1.
XX
PD 05-OCT-2000.
XX
PE 23-MAR-2000; 2000WO-US07723.
XX
PR 26-MAR-1999; 99US-0126506.
PR 07-JAN-2000; 2000US-0174852.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-611704/58.
DR P-PSDB; AAB45044.
XX
PT Nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT Parkinson's diseases and cancers -
XX
PS Claim 1a; Page 351-352; 418bp; English.
XX
CC This invention describes novel isolated nucleic acid molecules (I)
CC encoding a human secreted proteins (II) which have immunosuppressive,
CC antiarthritic, antirheumatic, antiproliferative, cytostatic, cardiant,
CC vasotropic, cerebroprotective, nootropic, neuroprotective, antibacterial,
CC virucide, fungicide, ophthalmological and vulnerary activity and can be
CC used for gene therapy. (I) and (II) are used to prevent, treat or
CC ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
CC horses, cats, dogs, chickens or sheep. (I) and (II) are also used in

CC diagnosing a pathological condition or susceptibility to a pathological
CC condition. The antibodies to (II) can also be used in alleviating
CC symptoms associated with the disorders and in diagnostic immunoassays
CC e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA).
CC Disorders which are diagnosed or treated include autoimmune diseases
CC e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms
CC of the breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous
CC system disorders e.g. Alzheimer's disease, infections caused by bacteria,
CC viruses and fungi and ocular disorders e.g. corneal infection. The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. The polypeptides can also be
CC used as a food additive or preservative to increase or decrease storage
CC capabilities.

XX
SQ Sequence 1537 BP; 378 A; 431 C; 352 G; 376 T; 0 other;

Query Match 86.3%; Score 16.4; DB 21; Length 1537;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGTCTGCAGCGGATGG 18
|||||
Db 1118 GGGTCTGCAGCTGGATGG 1101

RESULT 31
AAH65074

ID AAH65074 standard; DNA; 1824 BP.

XX AAH65074;

XX 26-SEP-2001 (first entry)

XX C glutamicum coding sequence fragment SEQ ID NO: 109.

XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.

XX Corynebacterium glutamicum.

XX EP108790-A2.

XX 20-JUN-2001.

XX 18-DEC-2000; 2000EP-0127688.

XX 16-DEC-1999; 99JP-0377484.

XX 07-APR-2000; 2000JP-0159162.

XX 03-AUG-2000; 2000JP-0280988.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX MPI; 2001-376931/40.

XX P-PSDB; AAG89855.

XX Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene

XX Claim 8; SEQ ID NO: 109; 246pp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived

CC from Coryneform bacterium, and identifying a homologue of a gene derived
CC from coryneform bacterium. Coryneform bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.

XX
SQ Sequence 1824 BP; 375 A; 466 C; 538 G; 445 T; 0 other;

Query Match 86.3%; Score 16.4; DB 22; Length 1824;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGTCTGCAGCGGATGGT 19
|||||
Db 301 GGTCTGCAGCGGAAGGT 318

RESULT 32
AAF71001

ID AAF71001 standard; DNA; 1947 BP.

XX AAF71001;

XX 30-APR-2001 (first entry)

XX C. glutamicum SRT protein nucleotide sequence SEQ ID NO:35.

XX Corynebacterium glutamicum; stress; resistance; tolerance; SRT;
KW fine chemical production; organic acid; proteinogenic amino acid;
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
KW carbohydrate; aromatic compound; vitamin; cofactor; polypeptide; enzyme;
KW evolutionary study; environmental hazard; fermentation; ds.

XX Corynebacterium glutamicum.

XX WO200100804-A2.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-IB00922.

XX 25-JUN-1999; 99US-0141031.

XX 01-JUL-1999; 99DE-1030429.

XX 01-JUL-1999; 99US-0142692.

XX 08-JUL-1999; 99DE-1031413.

XX 08-JUL-1999; 99DE-1031457.

XX 08-JUL-1999; 99DE-1031541.

XX 09-JUL-1999; 99DE-1032209.

XX 09-JUL-1999; 99DE-1032230.

XX 14-JUL-1999; 99DE-1032914.

XX 27-AUG-1999; 99DE-1040764.

XX 31-AUG-1999; 99DE-1041382.

XX (BADI) BASF AG.

XX Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G, Lee H;
PI Kim H;

XX MPI; 2001-061972/07.

XX P-PSDB; AAB78888.

XX New isolated Corynebacterium glutamicum nucleic acid encoding a stress,
PT tolerance or resistance protein, for production or modulation of
PT production of fine chemicals, such as, e.g. amino acids, lipids,
PT carbohydrates, or enzymes -

XX Claim 3; Page 166-169; 526pp; English.

CC AAF70984 to AAF71133 encode the Corynebacterium glutamicum stress,
CC resistance, and tolerance (SRT) proteins given in AAB78871 to AAB79020.
CC The C. glutamicum SRT genes (I) can be used in vectors (II) for
CC expression in host cells and production of fine chemicals, such as, an
CC organic acid, a proteinogenic or nonproteinogenic amino acid (preferred),
CC a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a
CC saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic
CC compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine
CC chemical production can be modulated. The presence of (I) or the SRT
CC proteins (III) encoded by them are used for diagnosing the presence
CC or activity of Corynebacterium diphtheriae. (I), (II), (III) and host
CC cells containing them can be used to map the genomes of organisms related
CC to C. glutamicum, to identify and localise C. glutamicum sequences of
CC interest, in evolutionary studies, in determination of SRT protein
CC regions required for function, in modulating the SRT protein activity,
CC and in modulating the activity of an SRT pathway. (II) are used to permit
CC C. glutamicum to survive in an environment that is normally
CC environmentally or chemically hazardous to it. (I) and protein molecules
CC encoded by it increase the survival of C. glutamicum to chemical and
CC environmental hazards and provide a means for continued growth and
CC multiplication in large scale fermentative growth conditions. By
CC increasing the growth rate or maintaining a normal growth rate in poor or
CC toxic conditions, the yield, production and/or efficiency or production
CC of fine chemicals from a culture may be increased.

XX SQ Sequence 1947 BP; 399 A; 502 C; 562 G; 484 T; 0 other;

Query Match 86.3%; Score 16.4; DB 22; Length 1947;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGCTGCAGCGGATGCT 19
|||
Db 401 GGCTGCAGCGGAGAGT 418

RESULT 33

ABL06358 ID ABL06358 standard; cDNA; 3309 BP.

XX AC ABL06358;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 13556.

XX KW Drosophila; developmental biology; cell signalling; insecticide;

XX KW pharmaceutical; gene; ss.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US09231.

XX PR 23-MAR-2000; 2000US-191637P.

XX PR 11-JUL-2000; 2000US-0614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li FWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR P-PSDB; ABB62255.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -

XX PS Claim 1; SEQ ID NO 13556; 21bp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (ABBS7737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 3309 BP; 878 A; 743 C; 832 G; 856 T; 0 other;

Query Match 86.3%; Score 16.4; DB 23; Length 3309;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGCTGCAGCGGATGCT 19
|||
Db 1319 GGCTGCAGCGGATGCT 1336

RESULT 34

AAV49652/C ID AAV49652 standard; DNA; 5802 BP.

XX AC AAV49652;

XX DT 23-OCT-1998 (first entry)

XX DE Human SRCR protein DNA.

XX KW Scavenger receptor cysteine rich domain; SRCR; diagnosis; treatment;

XX KW nervous system; medullo-blastoma; glioma; breast; detection;

XX KW autoantibody; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 107..5464

XX FT /*tag= a

XX FT /product= SRCR protein"

XX FT /note= "Scavenger receptor cysteine-rich domain

XX FT containing protein"

XX PN WO9830687-A2.

XX PD 16-JUL-1998.

XX PF 09-JAN-1998; 98WO-DE00096.

XX PR 18-JUL-1997; 97DE-1030997.

XX PR 09-JAN-1997; 97DE-1000519.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX PI Mollenhauer J, Poustka A;

XX DR WPI; 1998-399136/34.

XX DR P-PSDB; AAW64591.

PT Proteins containing scavenger receptor, cysteine rich domain -
PT useful for diagnosis and treatment of tumours

XX PS Claim 4; Fig 2; 54pp; German.

CC This sequence encodes a human protein which contains a SRCR (scavenger
CC receptor, cysteine-rich) domain. The gene and encoded protein can be used
CC to diagnose or treat tumours, particularly of the nervous system
CC (medullo-blastoma or glioma) or breast. The DNA sequence and probes
CC derived from it, are used to identify genes that express SRCR-domain
CC containing proteins, to determine the form in which these proteins exist

CC and to assess the significance of individual forms on cellular
CC properties. The protein can be used to detect the presence of
CC autoantibodies and antibodies which regulate its expression.
XX
SQ Sequence 5802 BP; 1253 A; 1614 C; 1576 G; 1359 T; 0 other;
Query Match 86.3%; Score 16.4; DB 19; Length 5802;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGTCTGCAGCGGATCG 18
Db 5435 GGGTCTGCAGCTGGATCG 5418
RESULT 35
AAS33414
ID AAS33414 standard; DNA; 8045 BP.
XX
AC AAS33414;
XX
DT 04-DEC-2001 (first entry)
XX
DE DNA encoding human secreted protein, Seq ID No 697.
XX
KW Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina;
KW rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmological;
KW cyostatic; Alzheimer's disease; Parkinson's disease; human; cancer;
KW multiple sclerosis; cancer; hyperproliferative disorder; infection;
KW Gaucher's disease; neurological disease; cerebrovascular disorder;
KW thrombosis; wound healing; ds.
XX
OS Homo sapiens.
XX
PN WO200155326-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01347.
XX
PR 31-JAN-2000; 2000US-0179065.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM,
XX
DR WPI; 2001-451931/48.
XX
PT New nucleic acids and polypeptides, useful for diagnosing, preventing
PT or treating medical conditions -
XX
PS Disclosure; SEQ ID No 697; 753bp; English.
XX
CC The invention relates to novel isolated nucleic acid molecules (I)
CC encoding human secreted proteins (II). (I) and (II) are used to prevent,
CC treat or ameliorate a medical condition in e.g. humans, mice, rabbits,
CC goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in
CC the prevention, treatment and diagnosis of diseases associated with
CC inappropriate expression of secreted proteins. (I) and complementary
CC sequences may also be used as DNA probes in diagnostic assays (e.g.
CC polymerase chain reactions (PCR)) to detect and quantitate the presence
CC of similar nucleic acid sequences in samples, and so which patients may
CC be in need of restorative therapy. (II) may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of the secreted
CC proteins. The anti-(II) antibodies and antagonists may also be used to
CC down regulate expression and activity of (II). The anti-(II) antibodies
CC may also be used as diagnostic agents for detecting the presence of (II)
CC in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The
CC disorders include for example: immune/autoimmune diseases (e.g. HIV
CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.

CC melanomas, neoplasms of the breast or liver, Sezary syndrome and
CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,
CC Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/
CC cerebrovascular disorders (e.g. cardiac arrest, tachycardia,
CC angina and thrombosis), infections caused by bacteria, viruses and
CC fungi and ocular disorders (e.g. corneal infections). (I) and (II),
CC agonists, antagonists and antibodies can also be used to promote wound
CC healing, maintain organs before transplantation, and support cell culture
CC of primary tissues. AAS33043-AAS33486 represent human secreted protein
CC coding sequences, PCR primers, and related sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification but was obtained in electronic format directly from WIPO
CC at: ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 8045 BP; 1257 A; 2365 C; 2854 G; 1569 T; 0 other;
Query Match 86.3%; Score 16.4; DB 22; Length 8045;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGTCTGCAGCGGATCG 18
Db 1232 GGGTCTGCAGCGGATCG 1249
RESULT 36
AAS33413
ID AAS33413 standard; DNA; 8047 BP.
XX
AC AAS33413;
XX
DT 04-DEC-2001 (first entry)
XX
DE DNA encoding human secreted protein, Seq ID No 696.
XX
KW Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina;
KW rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmological;
KW cyostatic; Alzheimer's disease; Parkinson's disease; human; cancer;
KW multiple sclerosis; cancer; hyperproliferative disorder; infection;
KW Gaucher's disease; neurological disease; cerebrovascular disorder;
KW thrombosis; wound healing; ds.
XX
OS Homo sapiens.
XX
PN WO200155326-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01347.
XX
PR 31-JAN-2000; 2000US-0179065.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM,
XX
DR WPI; 2001-451931/48.
XX
PT New nucleic acids and polypeptides, useful for diagnosing, preventing
PT or treating medical conditions -
XX
PS Disclosure; SEQ ID No 696; 753bp; English.
XX
CC The invention relates to novel isolated nucleic acid molecules (I)
CC encoding human secreted proteins (II). (I) and (II) are used to prevent,
CC treat or ameliorate a medical condition in e.g. humans, mice, rabbits,
CC goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in
CC the prevention, treatment and diagnosis of diseases associated with
CC inappropriate expression of secreted proteins. (I) and complementary
CC sequences may also be used as DNA probes in diagnostic assays (e.g.
CC polymerase chain reactions (PCR)) to detect and quantitate the presence
CC of similar nucleic acid sequences in samples, and so which patients may

CC be in need of restorative therapy. (II) may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of the secreted
CC proteins. The anti-(II) antibodies and antagonists may also be used to
CC down regulate expression and activity of (II). The anti-(II) antibodies
CC may also be used as diagnostic agents for detecting the presence of (II)
CC in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The
CC disorders include for example: immune/autoimmune diseases (e.g. HIV
CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
CC melanomas, neoplasms of the breast or liver, Sezary syndrome and
CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,
CC Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/
CC cerebrovascular disorders (e.g. cardiac arrest, tachycardia,
CC angina and thrombosis), infections caused by bacteria, viruses and
CC fungi and ocular disorders (e.g. corneal infections). (I) and (II),
CC agonists, antagonists and antibodies can also be used to promote wound
CC healing, maintain organs before transplantation, and support cell culture
CC of primary tissues. AAS33043-AAS33486 represent human secreted protein
CC coding sequences, PCR primers, and related sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification but was obtained in electronic format directly from WIPO
CC at: ftp.wipo.int/pub/published_pct_sequences.

CC SQ Sequence 8047 BP; 1258 A; 2367 C; 2853 G; 1569 T; 0 other;

Query Match 86.3%; Score 16.4; DB 22; Length 8047;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGTCTGCAGCGGGATGG 18
Db 1232 GGGTCTGCAGCGGGATGG 1249

RESULT 37

AAS59568
ID AAS59568 standard; DNA; 21719 BP.

XX AC AAS59568;

XX DT 13-FEB-2002 (first entry)

XX DE Propionibacterium acnes immunogenic protein encoding DNA #63.

XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant; ds.

XX OS Propionibacterium acnes.

XX PN WO200181581-A2.

XX PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US12865.

XX PR 21-APR-2000; 2000US-199047P.

XX PR 02-JUN-2000; 2000US-208841P.

XX PR 07-JUL-2000; 2000US-216747P.

XX PA (CORI-) CORIXA CORP.

XX PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX DR L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
CC treating acne vulgaris -

PS Claim 1; SEQ ID No 63; 1069pp; English.

XX Sequences AAS59506-AAS59804 represent DNA molecules encoding
CC Propionibacterium acnes immunogenic polypeptides. The proteins and their
CC associated DNA sequences are used in the treatment, prevention and
CC diagnosis of medical conditions caused by P. acnes. The disorders include
CC SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and
CC osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved
CC in infections of bone, joints and the central nervous system, however it
CC is particularly involved in the inflammatory lesions associated with acne
CC vulgaris. A method for detecting the presence or absence of P. acnes in a
CC patient comprises contacting a sample with a binding agent that binds to
CC the proteins of the invention and determining the amount of bound protein
CC in the sample. The polypeptides may be used as antigens in the production
CC of antibodies specific for P. acnes proteins. These antibodies can be
CC used to downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). This sequence encodes the
CC polypeptides shown in AAU55069-AAU55304 and AAU67565-AAU67566.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

CC SQ Sequence 21719 BP; 4285 A; 6649 C; 6206 G; 4578 T; 1 other;

Query Match 86.3%; Score 16.4; DB 23; Length 21719;
Best Local Similarity 94.4%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGTCTGCAGCGGGATGGT 19
Db 8274 GGCTCTGCAGCGGGATGGT 8291

RESULT 38

AAV49655/C
ID AAV49655 standard; DNA; 28720 BP.

XX AC AAV49655;

XX DT 23-OCT-1998 (first entry)

XX DE Human SC3 DNA.

XX KW Scavenger receptor cysteine rich domain; SRCR; diagnosis; treatment;
KW nervous system; medullo-blastoma; glioma; breast; detection; SC3;
KW autoantibody; ss.

XX OS Homo sapiens.

XX PN WO9830687-A2.

XX PD 16-JUL-1998.

XX PF 09-JAN-1998; 98WO-DE00096.

XX PR 18-JUL-1997; 97DE-1030997.

XX PR 09-JAN-1997; 97DE-1000519.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX PI Mollenhauer J, Poustka A;

XX DR WPI; 1998-399136/34.

PT Proteins containing scavenger receptor, cysteine rich domain -
PT useful for diagnosis and treatment of tumours

XX PS Disclosure; Fig 5c; 54pp; German.

CC This nucleotide sequence contains a fragment of a gene which is capable
CC of encoding a protein which contains a SRCR (scavenger receptor,

CC cysteine-rich) domain. The gene and encoded protein can be used to
CC diagnose or treat tumours, particularly of the nervous system
CC (medullo-blastoma or glioma) or breast. The DNA sequence and probes
CC derived from it, are used to identify genes that express SRCR-domain
CC containing proteins, to determine the form in which these proteins exist
CC and to assess the significance of individual forms on cellular
CC properties. The protein can be used to detect the presence of
CC autoantibodies and antibodies which regulate its expression.
XX
SQ Sequence 28720 BP; 6956 A; 6728 C; 6982 G; 8054 T; 0 other;

Query Match 86.3%; Score 16.4; DB 19; Length 28720;
Best Local Similarity 94.4%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGATGG 18
|||||
Db 28273 GGGTCTGCAGCTGGATCG 28256

RESULT 39
AAH64966/c
ID AAH64966 standard; DNA; 349980 BP.
XX
AC AAH64966;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 1.
XX
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-0127688.
XX
PR 16-DEC-1999; 99JP-0377484.
PR 07-APR-2000; 2000JP-0159162.
PR 03-AUG-2000; 2000JP-0280988.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
XX WPI; 2001-376931/40.
DR
XX
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
PT
XX
XX
PS Claim 7; SEQ ID NO: 1; 246bp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Coryneform bacterium, and identifying a homologue of a gene derived
CC from Coryneform bacterium. Coryneform bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX

SQ Sequence 349980 BP; 79703 A; 91547 C; 98381 G; 80349 T; 0 other;

Query Match 86.3%; Score 16.4; DB 22; Length 349980;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTCTGCAGCGGATGGT 19
|||||
Db 103135 GGTCTGCAGCGGAAGGT 103118

RESULT 40
AAZ56196
ID AAZ56196 standard; DNA; 19 BP.
XX
AC AAZ56196;
XX
DT 28-MAR-2000 (first entry)
XX
DE Oligonucleotide 110 for IL-3/IL-5/GM-CSF receptor expression inhibition.
XX
KW Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
KW asthma; allergy; cancer; receptor expression inhibitor; cytokine;
KW inflammation; hyper eosinophilia; eosinophil proliferation;
KW granulocyte macrophage colony stimulating factor; GM-CSF; ss.
XX
OS Homo sapiens.
XX
XX WO9966037-A2.
XX
PN 23-DEC-1999.
XX
PD 17-JUN-1999; 99WO-CA00572.
XX
PF 17-JUN-1998; 98CA-2235420.
XX
PR (REEX-) RECH EXPERTISES & DEV MEDICAUX PARENZ IN.
XX
PA Renzi P;
XX
PI WPI; 2000-097743/08.
XX
DR
XX
XX Antisense oligonucleotides directed to CCR3, interleukin or granulocyte
PT macrophage colony stimulating factor receptors, used for treating or
PT preventing asthma, allergies, hyper eosinophilia, inflammation or cancer
PT
XX
XX
PS Claim 5; Page 25; 72pp; English.
XX
XX This is an antisense oligonucleotide directed against the common beta
CC subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
CC receptor and the granulocyte macrophage colony stimulating factor
CC (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5
CC and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines
CC involved in eosinophil proliferation and survival, they are increased in
CC asthma and atopic diseases, and are also involved in the indefinite
CC proliferation of certain neoplastic diseases. The invention relates to
CC antisense oligonucleotides directed against a nucleic acid sequence
CC encoding either a chemokine receptor (CCR3), a common subunit of
CC interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common
CC subunit of IL-3, IL-5 and GM-CSF receptors. The antisense
CC oligonucleotides can be used in the treatment or prevention of asthma,
CC allergy, hyper eosinophilia, general inflammation or cancer.
XX
SQ Sequence 19 BP; 3 A; 4 C; 9 G; 3 T; 0 other;

Query Match 84.2%; Score 16; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCTGCAGCGGAT 16
|||||
Db 4 GGGTCTGCAGCGGAT 19

Wed Jan 14 07:58:27 2004

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Search completed: January 13, 2004, 18:02:39
Job time : 125.5 secs
